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Protein search results						
Search parameters		Search results				
Run on: June 14, 2004, 18:38:23 ; Search time: 18 Seconds (without alignments)						1220.756 Million cell updates/sec
Title: US-10-040-884-3 Exact score: 2192 Sequence: 1 MGMTRMLLECSLSDKLCVIQ.....LYAAVAGIRVESLFVNYSML 422						BLOSUM62
Scoring table: Gap0 10.0 , Gapext 0.5						gap
Total number of hits satisfying chosen parameters: 141681						141681
Minimum DB seq length: 0 Maximum DB seq length: 2000000000						length
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries						post-processing
Database: SwissProt_42.4*						database
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						Pred. No.
Summaries						summaries
Results						
No.	Score	Query Length	DB ID	Description		
1	446.5	20.4	B06	CEBK2 CHICK	P18460 gallus gallus	
2	444	20.3	B01	FGR3_MOUSE	P22607 mus musculus	
3	444	20.3	B01	FGR3_HUMAN	P22607 homo sapiens	
4	434	19.8	B02	FGR4_HUMAN	P22451 homo sapiens	
5	433	19.8	B21	FGR2_MOUSE	P21803 mus musculus	
6	428.5	19.5	B22	FGR1_MOUSE	P16029 mus musculus	
7	427.5	19.5	B08	FGR4_MOUSE	Q03142 mus musculus	
8	427	19.5	B21	FGR1_HUMAN	P21802 homo sapiens	
9	424	19.3	B19	FGR1_CHICK	P21804 gallus gallus	
10	424	19.3	B22	FGR1_HUMAN	P11362 homo sapiens	
11	419	19.1	B46	ABL_MLVAB	P00521 abelson murine	
12	419	19.1	B12	ABL1_MOUSE	P00520 mus musculus	
13	417	19.0	B130	ABL1_HUMAN	P00519 homo sapiens	
14	416	19.0	B21	FGR1_XENLA	P22192 xenopus laevis	
15	415	18.9	B22	FGR1_RAT	Q04589 rattus norvegicus	
16	415	18.9	B23	CEBK3_CHICK	P18461 gallus gallus	
17	407.5	18.6	B12	ABL1_HUMAN	P42684 homo sapiens	
18	403.5	18.4	B39	ABL_DROME	P10447 feline sarcoma virus	
19	397	18.1	B13	FGR2_XENLA	Q03364 xenopus laevis	
20	391	17.8	B138	TIE1_HUMAN	P35590 homo sapiens	
21	390	17.8	B134	TIE1_MOUSE	Q06806 mus musculus	
22	388	17.7	B29	FGR1_DROME	P07407 drosophila	
23	388	17.7	B136	TIE1_BOVIN	Q06805 bos taurus	
24	384	17.5	B20	ABL_DROME	P00522 drosophila	
25	382	17.4	B73	CD96_DROME	Q9vbv3 drosophila	
26	379	17.3	B06	SRA4_SPOUL	P42690 spongiformis	
27	376.5	17.2	B052	FGR2_DROME	Q09147 drosophila	
28	373	17.0	B370	SEA_AVIET	P23049 avian erythrocyte	
29	370.5	16.9	B25	TRICC_PIG	P24786 sus scrofa	
30	369	16.8	B92	FLT3_MOUSE	Q00342 mus musculus	
31	368.5	16.8	B224	ABL1_CAREL	P03949 caenorhabditis elegans	
32	367	16.8	B78	SEA_CHICK	Q91009 gallus gallus	
33	366	16.7	B115	RET_MOUSE	P03948 mus musculus	

RESULT_1			
CRK2_CHICK	STANDARD;	PRT;	806 AA.
ID CRK2_CHICK			
AC P18460;			
DT 01-NOV-1990 (Rel. 16, Created)			
DT 01-NOV-1990 (Rel. 16, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Tyrosine kinase receptor CRK2 precursor (EC 2.7.1.112).			
GN CRK2.			
OS Gallus gallus (Chicken).			
OC Gallirrotida; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC NCBI_TaxID=9031;			
OX [1]			
RN RP SEQUENCE FROM N.A.			
RX MEDLINE=903343672; PubMed=2165604;			
RA Pasquale E.B.;			
RT "A distinctive family of embryonic protein-tyrosine kinase receptors.";			
RT Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816 (1990).			
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.			
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC DR PIR: A35363; A35963; HSSP: P11362; 1FGK.			
CC DR InterPro: IPR007110; Ig-like.			
CC DR InterPro: IPR00598; Ig_C2.			
CC DR InterPro: IPR000719; Prot_kinase.			
CC DR InterPro: IPR01245; Tyr_Pkinase.			
CC DR InterPro: IPR008266; Tyr_Pkinase_AS.			
CC Pfam: PF00047; ig; 3.			
CC DR Pfam: PF00069; pkinase; 1.			
CC DR PRINTS: PR00109; TURKINSE.			
CC DR ProDom: PD000001; Prot_kinase; 1.			
CC DR SMART: SM00408; IGC2; 3.			
CC DR SMART; SM00219; TyrC; 3.			
CC DR PROSITE: PS50815; Ig_LIKE; 3.			
CC DR PROSITE; PS000710; PROTEIN_KINASE_ATP; 1.			
CC DR PROSITE; PS00107; PROTEIN_KINASE_DON; 1.			
CC DR PROSITE; PS50011; PROTEIN_KINASE_TIR; 1.			
CC DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferease; Phosphorylation; Transmembrane; Immunoglobulin domain; KW KW			

DR	SMART; SMART00408; IGC2; 3.			
DR	SMART; SMART00319; TyrKC; 1.			
DR	PS51835; Ig_LIKE; 3.			
PROSITE;	PS51835; Ig_LIKE; 3.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS01109; PROTEIN_KINASE_TYR; 1.			
Receptor;	Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain; Repeat; Signal; Alternative splicing.			
KW	Repeat; Signal; Alternative splicing.			
KW	POTENTIAL.			
RW	FT SIGNAL 1 20 FIBROBLAST. GROWTH FACTOR RECEPTOR 3.			
FT	CHAIN 21 801 TRICELLULAR (POTENTIAL).			
FT	DOMAIN 21 369 POTENTIAL.			
FT	TRANSMEM 370 390 CYTOPLASMIC (POTENTIAL).			
FT	DOMAIN 391 801 CYTOPLASMIC (POTENTIAL).			
FT	DOMAIN 39 123 IG-LIKE C2-TYPE 1.			
FT	DOMAIN 145 238 IG-LIKE C2-TYPE 2.			
FT	DOMAIN 247 349 IG-LIKE C2-TYPE 3.			
FT	DOMAIN 466 756 PROTEIN KINASE.			
FT	NP BIND 472 480 ATP (BY SIMILARITY).			
FT	BINDING 502 502 ATP (BY SIMILARITY).			
FT	ACT SITE 611 611 BY SIMILARITY.			
FT	MOD RES 642 642 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).			
FT	DISULFID 59 107 POTENTIAL.			
FT	DISULFID 170 222 POTENTIAL.			
FT	DISULFID 269 333 POTENTIAL.			
FT	CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	VARSPLIC 352 352 TAGANTDKLEEVLTDFEADGEYTLGAGNIGFSHS			
FT	AMVNLPL -> SWISENHPADARLIRANVSERDGEYFLCRA			
FT	TNF (GVAKAFFWLRVHGPQK. (in isoform 2).			
FT	/FTid=VP002390.			
FT	CONFICT 684 684 P -> L (IN REF. 2).			
FT	CONFICT 687 687 MISSING (IN REF. 2).			
SQ	SEQUENCE 801 AA; 87758 MW; 68BC110212691705 CRC64;			
Query Match	Best Local Similarity 20.3%; Score 444, DB 1, Length 801; Matches 120; Conservative 71; Mismatches 165; Indels 38; Gaps 10;			
Qy	34 VTFILLGVILWLFIREQRTQQRSGPQIAFP--PPPRDLSSWEAGRCGNVALPLKET 90			
Db	375 VVFELIVAAVILCRLSPPKGLGSPPVTKYTSRFPLKQVSLESMSMNNTPL--V 432			
Qy	91 SVENFLGATTPALA---KLQYP-----REQLSEVLEQICSGSCGFIFRANNMTGD 137			
Db	433 RIARLSSGEGPVLANVSELLELPADPKWELLRTRTLGKPGEGCFQVVAEAIGIDKR 492			
Qy	138 PSKPXSVLALKXEPAGLHEQDFLGRIQPHQYLGKHNVLQLEGCCTEKLPLIMVLEDY 197			
Db	493 TAKPTVAVKMLKDADTKLDSLVSEMEMKMKMCKHKNINLIGACTQGGLPVLYEA 552			
Qy	198 AQGDGILGFLWTCRDRDMTMGLL-----DLTKEVYHIGKVLLALEFLQEKHL 247			
Db	553 AKGNREFL-RARRP---FGMDYSFDACLPEEQLTCKLVSCAYQARGMEYIASQKC 607			
Qy	248 FGHDVAARNILMOSDILTAKLGLGLAYEVYTRGAISSTOF--IPLKWLAPERLILRPAST 305			
Db	608 IHRDLARNVLTVEDNMVKIADFLGLARDVNLDYYKXTNGRLPVKMAPALFDRVYH 667			
Qy	306 RADWNSFGILLYEMTGLGAP_PYPEPPPTSLIEHQLRKMKRPSQSCHTMYSTMKSCWR 364			
Db	668 QSDVNSFGVLUWEITPGGSPYGPVPELFKULLKEGHMDKPACTHOLYTMRECWH 727			
Qy	365 WREADPSPREIRLRLB--AAIKTADDEAVLQVP 396			
Db	728 AVPSQRPTFQLIVEDLDRILTVTSIDEYLISVP 761			
RESULT 3				

RA Superti-Furga A., Eich G., Bucher H.U., Wissner J., Giedion A.,
 RA Steinmann R., Steinmann B.;
 RT "A glycine 375-to-cysteine substitution in the transmembrane domain
 of the fibroblast growth factor receptor-3 in a newborn with
 achondroplasia.";
 RT Eur. J. Pediatr. 154:215-219 (1995).
 RL [10]
 RN VARIANT TD1 CYS-249.
 RX MEDLINE=96154693; PubMed=8589699.
 RA Tavormina P.L., Rimoin D.L., Cohn D.H., Zhu Y.-Z., Shiang R.,
 RA Wasman J.J.;
 RT "Another mutation that results in the substitution of an unpaired
 cysteine residue in the extracellular domain of FGFR3 in
 thanatophoric dysplasia type I.";
 RT Lachman R.S., Wilcox W.R., Thompson L.M., Zhu Y.-Z., Wilkin D.J.,
 RT Rimoin D.L., Cohn D.H., Wasman J.J.;
 RT mutations in fibroblast growth factor receptor 3."
 RL Hum. Mol. Genet. 4:2175-2177 (1995).
 RN [11]
 RP VARIANT HYPOCHONDROPLASIA LYS-540.
 RX MEDLINE=95400307; PubMed=7610477;
 RA Bellus G.A., McIntosh T.J., Smith E.A., Aylsworth A.S., Kaitila I.,
 RA Horton W.A., Greenhaw G.A., Hecht J.T., Francomano C.A.;
 RT "A recurrent mutation in the tyrosine kinase domain of fibroblast
 growth factor receptor 3 causes hypochondroplasia.";
 RL Nat. Genet. 10:357-359 (1995).
 RN [12]
 RP VARIANT CROUZON GLU-650.
 RX MEDLINE=95401326; PubMed=773297;
 RA Bellus G.A., McIntosh T.J., Smith E.A., Aylsworth A.S., Kaitila I.,
 RA Horton W.A., Greenhaw G.A., Hecht J.T., Francomano C.A.;
 RT "A recurrent mutation in the tyrosine kinase domain of fibroblast
 growth factor receptor 3 causes hypochondroplasia.";
 RL Nat. Genet. 9:321-328 (1995).
 RN [13]
 RP VARIANT CROUZON GLU-650.
 RX MEDLINE=96038601; PubMed=7610477;
 RA Meyers G.A., Orlova S.J., Munro I.R., Przybyla K.A., Jabs E.W.;
 RT "Fibroblast growth Factor receptor 3 (FGFR3) transmembrane mutation
 in Crouzon syndrome with acanthosis nigricans.";
 RL Nat. Genet. 11:462-464 (1995).
 RN [14]
 RP CHARACTERIZATION OF VARIANT ACH ARG-380.
 RX MEDLINE=96174812; PubMed=8599335;
 RA Webster M.K., Donoghue D.J.;
 RT "Constitutive activation of fibroblast growth factor receptor 3 by
 the transmembrane domain point mutation found in achondroplasia.";
 RL EMBO J. 15:520-527 (1996).
 RN [15]
 RP VARIANT TD1 CYS-248; CYS-249; CYS-370 AND CYS-373.
 RX MEDLINE=96254981; PubMed=8845844;
 RA Rousseau F., el Ghochi V., Delezoide A.L., Legrain-Mallet L.,
 RA Le Merrer M., Munirch A., Bonaventure J.;
 RT "Missense FGFR3 mutations create cysteine residues in thanatophoric
 dwarfism type I (TDI)." ;
 RL Hum. Mol. Genet. 5:509-512 (1996).
 RN [16]
 RP VARIANT CRS3 ARG-250.
 RX MEDLINE=97195561; PubMed=9042914;
 RA Muenke M., Gripp K.W., McDonald-McGinn D.M., Gaudenz K.,
 RA Whittaker L.A., Bartlett S.P., Markowitz R.I., Robin N.H., Nwokoro N.,
 RA Mulley J.J., Losken H.W., Mulliken J.B., Guttmacher A.E.,
 RA Wilroy R.S., Clarke L.A., Hollway G., Ades L.C., Haan E.A.,
 RA Mulley J.C., Cohen M.M., Jr., Bellus G.A., Francomano C.A.,
 RT "A unique point mutation in the fibroblast growth factor receptor 3
 (GFGR3) defines a new craniostenosis syndrome.";
 RL Am. J. Hum. Genet. 60:555-564 (1997).
 RN [17]
 RP VARIANT TD1 CYS-370.
 RX MEDLINE=98004917; PubMed=9790257;
 RA Karsumata N., Kuno T., Miyazaki S., Mikami S., Nagashima-Miyokawa A.,
 RA Niimura A., Horikawa R., Tanaka T.;
 RT "G370C mutation in the FGFR3 gene in a Japanese patient with
 thanatophoric dysplasia.";
 RL Endocr. J. 45:S171-S174 (1998).

RN [18] VARIANT HYPOCHONDROPLASIA VAL-538.
 RP Grigelionene G., Hadenaas L., Ekloef O., Neumeyer L., Haereid P.E.,
 RA Arvert M.;
 RT "A novel missense mutation Ile538Val in the fibroblast growth
 factor receptor 3 in hypochondroplasia.";
 RL Hum. Mutat. 11:333-333 (1998).
 RN [19]
 RP VARIANT HYPOCHONDROPLASIA THR-540.
 RX MEDLINE=98112422; PubMed=9420433;
 RA Deutz-Terlouw P.P., Loskoot M., Alafs C.M., Hennekam R.C.M.,
 RA Baker E.;
 RT "Ans50thr substitution in the fibroblast growth factor receptor 3
 tyrosine kinase domain causing hypochondroplasia.";
 RL Hum. Mutat. 12:562-565 (1998).
 RN [20]
 RP VARIANT TD1 MET-650.
 RX MEDLINE=99400545; PubMed=10471491;
 RA Kitoh H., Brodie S.G., Kupke K.G., Lachman R.S., Wilcox W.R.,
 RA Capellen D., De Oliveira C., Ricci D., Gil Diez de Medina S.,
 RA Bourdin J., Sabre-Garaix X., Chopin D., Thiry J.P., Radvanyi F.,
 RT "Frequent activating mutations of FGFR3 in human bladder and cervix
 carcinomas";
 RL Nat. Genet. 23:18-20 (1999).
 CC -!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.
 CC -!- PREFERENTIALLY BINDS FGFR1;
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -!- tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC -!- Event-Alternative splicing; Named isoforms=3;
 CC -!- Name=1; Synonym=IIIC;
 CC -!- IsoId=P22607-1; Sequence=Displayed;
 CC -!- Name=2; Synonym=I; Irbp;
 CC -!- IsoId=P22607-2; Sequence=vSP_002988;
 CC -!- Name=3;
 CC -!- IsoId=P22607-3; Sequence=vSP_002989;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, KIDNEY AND TESTIS. VERY
 CC -!- LOW OR NO EXPRESSION IN SPLEEN, HEART, AND MUSCLE. IN 20- TO 22-
 CC -!- WEEK OLD PUPES IT IS EXPRESSED AT HIGH LEVEL IN KIDNEY, LUNG,
 CC -!- SMALL INTESTINE AND BRAIN, AND TO A LOWER DEGREE IN SPLEEN, LIVER,
 CC -!- AND MUSCLE. EPITHELIAL CELLS SHOW EXCLUSIVELY ISOFORM 2
 CC -!- TRANSCRIPTS WHILE FIBROBLASTIC CELLS SHOW A MIXTURE OF ISOFORMS 1
 CC -!- AND 2. TRANSCRIPTS.
 CC -!- DISEASE: Defects in FGFR3 are the cause of achondroplasia (ACH)
 CC -!- [MIM:100800]. ACH is an autosomal dominant disease and is the most
 CC -!- frequent form of short-limb dwarfism. It is characterized by a
 CC long, narrow trunk, short extremities, particularly in the
 Query Match 20.3%; Score 444; DB 1; Length 806;
 Best Local Similarity 30.5%; Pred. No. 2e-26;
 Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;
 QY 34 VTFIPLLGVTLWLFIREQRTQQRSGP---QGIAAPVPPPRDLWSAGHGGNVNALPL-KE 89
 DB 381 VGFELTILVVAATVLCRLLRSPPKKGSPTVHKLRSRFLPLKPLSEASMSNTPLVRL 440
 QY 90 TSVENFLGLATTPAKLQLQP-----REQLSEVLEQJCSGCGPFRANNNTGDP 139
 DB 441 ARLSSEGEGPILANVSEELPADPKWELSLRALTGKPLSGEGCQGVVMAEAGIDKDRA 500
 QY 140 KPKSTVILKALKREPAGLHEVQDFGRIGIQFHOLYGRKHKNLYQLEGCCTEKLPFLYMLVEDAQ 199
 DB 501 KPVTVAVOMLKDDATDKDLSLVLSEMEMKKMIGRKHNINLGLACTQGGPLYLVLEYAAK 560
 QY 200 GDLIGFLWTRDWTMDGLY-----DLTEKQVYHIGQCVLLALEFLQKHLFH 249

Db	561	GNLREFL-RASRP---PGDYSFEDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCTH	615	Schnierch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Qy	250	GDVAARNILMOSDLTAKLGCLGLAYEVYTRGAISSSTOT--IPLKWLAPERLLRPAStRA	307	[5]
Db	616	RDLAARNVLTEDDNVNMKIADGFGLARDVHNLDDYKKTCNTGRLPVKWNAPEAFDRYTHQS	675	SEQUENCE OF 609-676 FROM N.A.
Qy	308	DWWSFGVILYENVTGKAPPVPPPTSLILEHLQRRIKMKRPSCTHTMYSIMKSWRMRE	367	TISSUE=Blood; RX
Db	676	DWWSFGVILWETFLGGSPYPolPVEELFKLLEKGHRMDKFANCIDLYMIMRECWAAP	735	RT "Putative Tyrosine kinase expressed in K-562 human leukemia cells.";
Qy	368	ADRPSPREBLRLRLEAAIK-TADDE	390	Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917 (1990).
Db	736	SQRPTRKQLVEDLDRVLTIVTSD	759	-!- FUNCTION: RECEPTOR FOR ACIDIC FIBROBLAST GROWTH FACTOR. DOES NOT BIND TO BASIC FIBROBLAST GROWTH FACTOR. BINDS FGFR9.
				-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
				-!- SUBCELLULAR LOCATION: Type I membrane protein.
				-!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.
				-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
				CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
				CC DR EMBL: X57205; OAA40490_1; -.
				CC DR EMBL: L03840; PAB59389_1; -.
				CC DR EMBL: Y13901; CRA7420_1; -.
				CC DR EMBL: M59373; AAA63208_1; -.
				CC DR PIR: S15345; TTHUFA4.
				CC DR PDB: 1QCT; 15-TUN-99.
				CC DR Genew: HGNC:3691; FGFR4.
				CC DR MIM: 134935; -.
				CC DR GO; GO:0005007; C:integral to plasma membrane; TAS.
				CC DR GO; GO:0008543; F:fibroblast growth factor receptor activity; TAS.
				CC DR InterPro: IPR01110; Ig-like.
				CC DR InterPro: IPR033598; Ig_C2.
				CC DR InterPro: IPR00719; Prot_kinase.
				CC DR InterPro: IPR01245; TYR_Pkinase.
				CC DR InterPro: IPR08266; TYR_Pkinase_AS.
				CC DR Pfam: PF00047; ig_3.
				CC DR Pfam: PF00069; pkinase_1.
				CC DR PRINTS: PR00109; TYRKINASE.
				CC DR Prodrom: P000001; Prot_kinase_1.
				CC DR SMART: SM00408; IgC2_3.
				CC DR SMART: SM00219; TyrIC_1.
				CC DR PROSITE: PS50085; Ig_LIKE_2.
				CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
				CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
				CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
				CC KW Receptor; Glycoprotein; Tyrosine_protein_kinase; ATP-binding; Transferease; Phosphorylation; Transmembrane; Immunoglobulin domain; Repeat; Signal; Polymorphism; 3D-structure.
				CC KW SIGNAL 1 24
				CC FT CHAIN 25 802
				CC FT DOMAIN 25 369
				CC FT TRANSMEM 370 390
				CC FT DOMAIN 399 802
				CC FT DOMAIN 30 128
				CC FT DOMAIN 152 240
				CC FT DOMAIN 249 349
				CC FT DOMAIN 467 755
				CC FT DOMAIN 473 481
				CC FT BINDING 503 503
				CC FT ACT_SITE 612 612
				CC FT MOD_BES 643 643
				CC FT DISULFID 57 101
				CC FT DISULFID 172 224

Query Match 19.8%; Score 434; DB 1; Length 802;
Best Local Similarity 29.8%; Pred. No. 1.2e-25;
Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

QY 21 EKQEVEVIV--PFLVLTIFPLLGVLWLFIREQTQDQRSGP---QGIAVPPPPDLDL 73
Db 364 EARATDILLYIASGLALAVILLAGL---YRQALGRHPRPPATTQKLRSRPLAQF 418

QY 74 SWEAQHGGNVALPPL-KETSVENFLGATTPALAKQVPREQSE-----VL-EQICSSC 125
Db 419 SLESGSSGKSSSSSLVRGVLSSSOPALLAGLVSIDLPIDPLWEPFDRLVLRGPLGEGCF 478

QY 126 GPITPRANNMTGDPSPKP---KSVVILKALKEPAQHLBVDQLFLGRTOFHQIGKHNLYQDEG 182
Db 479 QGVTRAAFGMDPAPRDQSTVAKMILDNASDKDLADLSEMEVMKLGHRHNINLIG 538

QY 183 CCTCEKPLPMLVNLVEDVAGQDILGFLWTCTRDV---MTMDG-----LIVDYLTEKQVYHIG 232
Db 539 VCTORGPLPVIVEAAGKNLREFL-RARPPGPDSLSPDRSSRGPLSPVLYVSCAY --- 594

QY 233 KQVLLALEFLQEKHLFHGDVAARNILMQMSDLTAKLCGLAYEVYTRAISSSTQ---IPL 290
Db 595 -QVARGMTCYLESRCIHDLAARNIVLVTEDVNMKIADFGLARGYHIIQYKKTNSGRIPV 653

QY 291 KWVAPERLLRPSAIRADWVSGFLLYENVTLGAPPYEVPPPSILEHQRRKIMKRSS 350
Db 654 KWVAPPEALFDRVYTHOSDWFSGLWELFTLGSPSPYCPVPEELFLSREGRHMRDLPBH 713

QY 351 CTHTMYSIMKSCWRWREADRPSPELRLREAALKTDADE 390
Db 714 CPPBLYGMRECWAAPSORPTFKQLVVAELDKVLLAVSEE 753

RESULT 5

FGFR2_MOUSE STANDARD; PRT; 821 AA.
AC P21803; O55141; Q001389; Q61342;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (Keratinocyte growth factor receptor 2 precursor (EC 2.7.1.112) (FGFR-2))
GN FGFR2 OR ECFL OR BEK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TAXID=10090;
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RP TISSUE=Brain; and Liver;
RX MEDLINE:92228773; PubMed=1373495;
RA Mansukhani A., Dell'Era P., Moscatelli D., Korbluth S.,
RA Hanausa H., Basilio C.,
RR "Characterization of the murine BEK fibroblast growth factor (FGF) receptor: activation by three members of the FGF family and requirement for heparin.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3305-3309(1992).
RN SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE:91270892; PubMed=1711190;
RA Raz V., Kelman Z., Avivi A., Neufeld G., Givoli D., Yarden Y.,

[1] Sequence from N.A. (ISOFORM LONG).
RN SEQUENCE FROM N.A. (ISOFORM SHORT).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE:91095977; PubMed=1846048;
RA Miki T., Fleming T.P., Bottaro D.P., Rubin J.S., Ron D.,
RA Aaronson S.A.;
RA "Expression cDNA cloning of the KGF receptor by creation of a transforming autoocrine loop.";
RT "Expression cDNA cloning of the KGF receptor by creation of a transforming autoocrine loop.";
RN Science 251:72-75(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE:98167854; PubMed=9-99422;
RA Twigg S.R.F., Burns H.D., Oldridge M., Heath J.K., Wilkie A.O.M.;
RT "Conserved use of non-canonical 5' splice site (GA) in alternative splicing by fibroblast growth factor receptors 1, 2 and 3.";
RL Hum. Mol. Genet. 7:685-691(1998).
RN [5]
RP SEQUENCE OF 477-821 FROM N.A.
RC TISSUE=Liver
RX MEDLINE:8-9219016; PubMed=2468999;
RA Korbluth S., Paulson K.E., Hanusa H.;
RT "Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA libraries";
RT Mol. Cell. Biol. 8:5541-5544 (1988).
CC -!- FUNCTION: RECEPTOR FOR BASIC FGF/S.
CC -!- POSSESSES A HIGHER AFFINITY FOR ACIDIC THAN FOR BASIC FGF/S.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoID=P21803-1; Sequence=Displayed;
CC Name=Short;
CC IsoID=P21803-2; Sequence=VSP_002985; VSP_002986; VSP_002987;
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC DR M86441; AAA37286; 1;-.
CC DR X55441; CAA3908; 1;-.
CC DR M63503; AAA39377; 1;-.
CC DR Y16152; CAA76098; 1;-.
CC DR Y16167; CAA16099; 1;-.
CC DR M23362; AAA37285; 1;-.
CC DR P1R; A44142; TMSBK.
CC DR P1R; S17295; S17295.
CC DR HSSP; P11362; 1FGR.
CC DR M61; 955523; Egfr2.
CC DR GO:0007433; P:salivary gland morphogenesis; IMP.
CC DR InterPro; IPR007110; Ig-1-like.
CC DR InterPro; IPR003598; Ig_c2.
CC DR InterPro; IPR000119; Prok_kinase.
CC DR InterPro; IPR001245; Tyr_Pkinase.
CC DR InterPro; IPR008266; Tyr_Pkinase_AS.
CC DR PFM; PF00047; Ig; 3.
CC DR PRINTS; PRO00109; TYRKINASE.
CC DR ProdDom; PD00001; Prok_kinase; 1.
CC DR SMART; SM00408; IgC2; 3.
CC DR SMART; SM00219; TyrKc; 1.
CC DR PROSITE; PSS0035; Ig_LIKE; 3.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

family, expressed in the definitive endoderm and skeletal muscle lineages of the mouse.";
Development 113:641-651 (1991).

[2] SEQUENCE OF 620-676 FROM N.A.
STRAIN=C57BL/6; TISSUE=Embryonic brain;
MEDLINE=93036484; Published=1281307;

C Heinenstein P., Nieto M.A., Frain M., Mattei M.-G.,
A Chastier A., Wilkinston D.G., Charney P.;
A "An Eph-related receptor protein tyrosine kinase gene segmentally
expressed in the developing mouse hindbrain.";
T Oncogene 7:2499-2506(1992).

C -!- FUNCTION: PUTATIVE RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
C MAY BE INVOLVED IN THE DEVELOPMENT OF SKELETAL MUSCLE CELL
C LINEAGES.

C -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
C tyrosine phosphate.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING GUT ENDODERM,
C IN MYOTOMALLY DERIVED SKELETAL MUSCLE, THE ADRENAL CORTEX,
C KIDNEY AND CONDENSING CARTILAGE. PRESENT IN ADULT LIVER,
C LUNG AND KIDNEY.

C -!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.

C -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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C EMBL; X59927; CAA42551.1; .
 C EMBL; X57236; CAA40512.1; .
 R PIR; S18209; S18209.
 R HSSP; P11362; IPRK.
 R MGD; MGI: 955225; RGfr4.
 R InterPro; IPR007110; Ig-like.
 R InterPro; IPR003538; Ig_c2.
 R InterPro; IPR000719; Prot_kinase.
 R InterPro; IPR001245; Tyr_kinase.
 R InterPro; IPR008266; Tyr_pk kinase_AS.
 R Pfam; PF00047; Ig_3.
 R Pfam; PF00069; Phinase; 1.
 R PRINTS; PRO0109; TYRKINASE.
 R PRODOM; PD000001; Prot_kinase; 1.
 R SMART; SM00408; IGC2; 3.
 R SMART; SM0019; Tyrc; 1.
 R PROSITE; PS00835; Ig_LIKE; 2.
 R PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 R Receptor; Glycoprotein; Tyrosine_protein_kinase; ATP-binding;
 R Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
 R Repeat; Signal; .
 R SIGNAL; 1 18 POTENTIAL.
 R CHAIN 19 808 FIBROBLAST GROWTH FACTOR RECEPTOR_4.
 R DOMAIN 19 366 EXTRACELLULAR (POTENTIAL).
 R TRANSEM 367 387 POTENTIAL.
 R DOMAIN 388 808 CYTOPLASMIC (POTENTIAL).
 R DOMAIN 53 138 IG-LIKE C2-TYPE 1.
 R DOMAIN 149 237 IG-LIKE C2-TYPE 2.
 R DOMAIN 246 346 IG-LIKE C2-TYPE 3.
 R DOMAIN 464 761 PROTEIN KINASE.
 R NP BIND 470 478 ATP (BY SIMILARITY).
 R BINDING 509 509 ATP (BY SIMILARITY).
 R ACT_SITE 618 618 BY SIMILARITY.
 R MOD_RES 649 649 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 R DISTIFID 53 98 POTENTIAL.
 R DISULFID 169 221 POTENTIAL.
 R DISULFID 268 330 POTENTIAL.

- genome.";
 Proc. Natl. Acad. Sci. U.S.A. 87:8180-8184 (1990).
 [31]
- SEQUENCE FROM N.A. (ISOFORM 17).
 MEDLINE=91274356; PubMed=1647213;
- RX Sano M., Sasada R., Watanabe T., Ishimaru K., Igarashi K., "Two cDNAs encoding novel human EGFR receptor.";
 RT Biochim. Biophys. Acta 1083:244-246 (1991).
 [4]
- RN RP SEQUENCE FROM N.A. (ISOFORM 4).
 TISSUE=Stomach cancer;
 MEDLINE=90332706; PubMed=2377625;
- RX Hattori Y., Odagiri H., Nakatani H., Miyagawa K., Naito K., Sakamoto H., Katcho O., Yoshiida T., Sugimura T., Terada M.;
 RA RT "K-sam, an amplified gene in stomach cancer, is a member of the RT heparin-binding growth factor receptor genes";
 RT proc. Natl. Acad. Sci. U.S.A. 87:5983-5987(1990).
 [5]
- RN RP SEQUENCE FROM N.A. (ISOFORMS 5; 14 AND 15).
 MEDLINE=92212946; PubMed=1313574;
- RX RA Kato M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y., Sugimura T., Terada M.;
 RA RT "K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase.";
 RT proc. Natl. Acad. Sci. U.S.A. 89:2960-2964 (1992).
 [6]
- RN RP SEQUENCE FROM N.A. (ISOFORM 3).
 TISSUE=Placenta;
 MEDLINE=93016048; PubMed=1400433;
- RX Dell K.R., Williams L.T.;
 RT "A novel form of fibroblast growth factor receptor 2. Alternative splicing of the third immunoglobulin-like domain confers ligand binding specificity.";
 RT proc. Natl. Acad. Sci. U.S.A. 89:21225-21229(1992).
 [7]
- RN RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 19), AND VARIANT ARG-613.
 TISSUE=Mammary gland;
 MEDLINE=92108030; PubMed=1309608;
- RX RA Miki T., Boccardo D.P., Fleming T.P., Smith C.L., Burgess W.H., Chan A.M.-L., Aaronson S.A.;
 RT "Determination of ligand-binding specificity by alternative splicing: two distinct growth factor receptors encoded by a single gene.";
 RT proc. Natl. Acad. Sci. U.S.A. 89:246-250(1992).
 [8]
- RN RP SEQUENCE FROM N.A. (ISOFORM 19).
 TISSUE=Breast, and Cornea;
 MEDLINE=95170769; PubMed=866434;
- RX RA Wilson S.E., Wang J., Chwang E.L., Gollahan L., Leitch A.M., Shay J.W.;
 RT "Hepatocyte growth factor (HGF) keratinocyte growth factor (KGF), and their receptors in human breast cells and tissues: alternative receptors.";
 RT Cell. Mol. Biol. Res. 40:337-350(1994).
 [9]
- RN RP SEQUENCE FROM N.A. (ISOFORM 7; 9; 10; 11; 12 AND 13), AND VARIANT ERATOM.
 TISSUE=Breast, and Cornea;
 MEDLINE=20090220; PubMed=10626794;
- RX RA Steinberger D., Mueller U.; Steinberger D., Mueller U.;
 RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 [11]
- RN RP SEQUENCE FROM N.A. (ISOFORMS 7; 9; 10; 11; 12 AND 13), AND VARIANT ARG-613.
 TISSUE=Blood;
- RX RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibusawa T., Sakamoto H., Ishii H., Yanagihara K., Maefusa K., Terada M.;
 RA RT "Deletion of the carboxy-terminal exons of K-sam/FGFR2 by short homology-mediated recombination, generating preferential expression of specific messenger RNAs.";
 RT Nat. Genet. 8:98-103 (1994).
- RL RN Cancer Res. 59:6080-6086 (1999).
 [12]
- SEQUENCE FROM N.A. (ISOFORMS 5; 6; 8; 14 AND 18).
 RX MEDLINE=21845873; PubMed=1185667;
- RX Ingersoll R.G., Paznaskas W.A., Tran A.K., Scott A.F., Jiang G., Jabs B.W.;
 RT "Fibroblast growth factor receptor 2 (FGFR2): genomic sequence and variations";
 RT Cytogenet. Cell Genet. 94:121-126(2001).
 RN [13]
- SEQUENCE FROM N.A. (ISOFORM 3).
 RX Lind D.L., Cox D.R.;
 RT "Sequence and polymorphisms in fibroblast growth factor receptor 2 (FGFR2) Gene in humans";
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [14]
- SEQUENCE OF 314-427 FROM N.A.
 RX MEDLINE=20177482; PubMed=10712195;
- RX Glaser R.L., Jiang W., Boyadjiev S.A., Tran A.K., Zachary A.A., van Maldergem L., Johnson D., Walsh S., Oldridge M., Wall S.A., Wilkie A.O.M., Jabs E.W.;
 RT "Paternal origin of FGFR2 mutations in sporadic cases of Crouzon syndrome and Pfeiffer syndrome.";
 RT Am. J. Hum. Genet. 66:768-777 (2000).
 RN [15]
- SEQUENCE OF 1-209; 212-767 AND 771-821 FROM N.A. (ISOFORMS 5; 14 AND 18).
 RP RP SEQUENCE OF 99214070; PubMed=10196476;
- RX Zhang Y., Gory M.C., Post J.C., Ehrlich G.D.;
 RT "Genomic organization of the human fibroblast growth factor receptor 2 (FGFR2) gene and comparative analysis of the human FGFR gene family.";
 RT Gene 230:69-79 (1999).
 RN [16]
- RP SEQUENCE OF 249-313; AND VARIANTS AS TRP-252 AND ARG-253.
 RX MEDLINE=9539781; PubMed=7668257;
- RX Park W.-J., Theda C., Maestri N.E., Meyers G.A., Fryburg J.S., Dufrene C., Cohen M.M. Jr., Jabs E.W.;
 RT "Analysis of phenotypic features and FGFR2 mutations in Apert syndrome.";
 RT Am. J. Hum. Genet. 57:321-328(1995).
 RN [17]
- RP SEQUENCE OF 251-259 FROM N.A.
 RX MEDLINE=96753074; PubMed=8676562;
- RX Wada C., Ishigaki M., Toyo-oka Y., Yamabe H., Ohnuki Y., Takada F., Yamazaki Y., Ohnami H.;
 RA RT "Nucleotide sequences at intron 6 and exon 7 junction of fibroblast growth factor receptor 2 and rapid mutational analysis in Apert syndrome.";
 RT Rinsho Byori 44:435-438 (1996).
 RN RP SEQUENCE OF 251-318 FROM N.A.
 RX MEDLINE=96241572; PubMed=8673103;
- RX Moloney D.M., Slaney S.F., Oldridge M., Wall S.A., Sahlin P., Sterman G., Wilkie A.O.M.;
 RT "Exclusive paternal origin of new mutations in Apert syndrome.";
 RT RL Nat. Genet. 13:48-53(1996).
 RN [18]
- RP SEQUENCE OF 263-361 FROM N.A., AND VARIANT CS PRO-289; ARG-338;
 RX MEDLINE=96090259; PubMed=7581378;
- RX Gory M.C., Preston R.A., White G.J., Zhang Y., Singhvi V.K., Losken H.W., Parker M.G., Nwokoro N.A., Post J.C., Ehrlich G.D.;
 RA RT "Crouzon syndrome: mutations in two spliceforms of FGFR2 and a common point mutation shared with Jackson-Weiss syndrome.";
 RT RL Hum. Mol. Genet. 4:1387-1390(1995).
 RN [19]
- RP SEQUENCE OF 200-342; TYR-342; GLY-344 AND CYS-354.
- RX MEDLINE=95078932; PubMed=7987400;
- RX Reardon W., Winter R.M., Rutland P., Pulley L.J., Jones B.M., Malcom S.;
 RA RT "Mutations in the fibroblast growth factor receptor 2 gene cause Crouzon syndrome.";
 RT Nat. Genet. 8:98-103 (1994).
- RN [20]

RN	[21]	VARIANTS CS CYS-328 AND CYS-347, AND VARIANT JWS GLY-344.	RX	MEDLINE=89315814; PubMed=2473471;
RP		Pasquale E.B.; Singer S.J.;	RA	"Identification of a developmentally regulated protein-tyrosine kinase by using anti-phosphotyrosine antibodies to screen a cDNA expression library";
RX	Medline=50179174; PubMed=7874170;	RT	Proc. Natl. Acad. Sci. U.S.A. 86:5449-5453 (1989).	
RA	Jabs E.W., Li X., Scott A.F., Meyers G.A., Chen W., Eccles M., Mao J.,	RT	[2]	
RA	Charnas L.R., Jackson C.E., Jaye M.;	RL	Nat. Genet. 8:275-279(1994).	
RA	"Jackson-Weiss and Crouzon syndromes are allelic with mutations in fibroblast growth factor receptor 2.";	RP		
RT	REVISONS.	RP		
RN	[22]	Variants CS.	RA	Pasquale E.B.;
RP		Submitted (May-1989) to the EMBL/GenBank/DBJ databases.	RL	Submitted (May-1989) to the EMBL/GenBank/DBJ databases.
RN		[3]	RN	
RA	Oldridge M., Willkie A.O.M., Staney S.F., Poole M.D., Pulley L.J., Rutland P., Hockley A.D., Wake M.J.C., Goldin J.H., Winter R.M.,	RP	SEQUENCE FROM N.A.	
RA	Reardon W., Malcolm S.;	RX	MEDLINE=89398406; PubMed=2544996;	
RA	"Mutations in the third immunoglobulin domain of the fibroblast factor receptor-2 gene in Crouzon syndrome.";	RA	Lee P.L., Johnson D.B., Cousins L.S., Fried V.A., Williams L.T.	
RT	RT fibroblast growth factor receptor for basic fibroblast growth factor.";	RT	"Purification and complementary DNA cloning of a receptor for basic fibroblast growth factor.";	
RN	[23]	Science 245:57-60 (1990).	RT	Science 245:57-60 (1989).
RP	VARIANTS CS GLY-290; TRP-342 AND CYS-354, AND VARIANT JWS ARG-342.	CC	-!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.	
RX	Medline=613301; PubMed=85221214;	CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.	
RA	Park W.-J., Meyers G.A., Li X., Theda C., Day D., Orlow S.J., Jones M.C., Jabs E.W.;	CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.	
RA	"Novel FGFR2 mutations in Crouzon and Jackson-Weiss syndromes show RT	CC	-!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.	
Query Match	19.5%; Score 427, DB 1, Length 821.	CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.	
Best Local Similarity	27.4%; Pred. No. 4.2e-25;	CC		
Matches	115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
Qy	22 KQVENTIVPPLL-----VTFPLILGLVWLFIREQRTQQRSPOGIA-----PV 67	CC	EMBL: M24637; AAA8663.1; -.	
Db	3.65 REKEITASPDYLETAIYCIGVFLIAACMVTYVILCRMKNTKKPDESSOPAVHKLTKRIPL 424	CC	PIR: P11345; TVCHFG.	
Qy	68 PPPRDLSWEAGHGGNVALPILKETSYENFLGATTPALA-----KLQVPREQLSEV 116	CC	HSSP: P11362; FGK.	
Db	425 RRQTVSAE5555MSMNNTPLVPRITRLLSSADTPMLAGSBEYELPDPKWBPFRDKLT-L 483	CC	InterPro: IPRO07110; Ig-like.	
Qy	117 LEQICGSGCCPIFRANMNTGDPSPK-----SVLKALKEPAGLHEVDFLGRIOFPHQYLGK 173	CC	InterPro: IPRO03598; Ig_c2.	
Db	484 GKPLGEKGCFQVVMAAEVGIDKDKDKEAVYAVKMLKDDETEKDSLYSEMENMKMIGK 543	CC	InterPro: IPRO07129; Prot_kinase.	
Qy	174 HKNLVQLEGGCTEKPLWYLEDVAQGDLLGFLWTQDWTMDGLYD-----LTE 225	CC	InterPro: IPRO01245; Tyr_P kinase.	
Db	544 HKNINLNLLGACTQDGPLYVVEYASKGNLREYLARRPPGMEYS--YDINRVPPEQMTF 600	CC	InterPro: IPRO08266; Tyr_pk kinase_AS.	
Qy	226 KQVTHIGKQVLLALEFLQEGKHLFHGDVVAARTNLIMOSDLTAKLCGHGLA-----YEYV 277	CC	PRINTS: PRO0169; pkinase; 1.	
Db	601 KDLVSCTYQLARGMEYLASSQKICIRDLAARNVLVTTNNYKIAIDGLARDINNDYYKCT 660	CC	ProDom: PD000001; Prot kinase; 1.	
Qy	278 TRGALSSTQTPLKWLAPERULLRPARSIRADWVSSGFLYEMVTLGAPPVPEVPPTSILE 337	CC	SMART: SM00408; IgG2; 3.	
Db	661 TNG-----FLPVKVNAAPEALFDRYVDTQSDWPSQVLMETIFLUGGSPPGIPVBELPK 714	CC	DR	
Qy	338 HLRQRKIMKRPSSCSTHTMYM1MSKCSWRARRADRSPSPRELRLERAAKTDADDAEVLQVPE 397	CC	PROSTE: PS05035; IG_LIKE; 3.	
Db	715 LLKEGHRMDDPANCNTNELMMRDCWHAVSQSRPFTFKOLVEDDLRILTLTNEEYLDLSQ 774	CC	DR	
		FT	PROSTE: PS01017; PROTEIN_KINASE_ATP; 1.	
		FT	PROSTE: PS50011; PROTEIN_KINASE_DOM; 1.	
		FT	PROSTE: PS05019; PROTEIN_KINASE_TYR; 1.	
		KW	Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transfere; Phosphorylation; Transmembrane; Signal.	
		KW	Receptor; Signal; Transmembrane; Immunoglobulin domain.	
		FT	POTENTIAL_SIGNAL 1 21	
		FT	POTENTIAL_CHAIN 22 819	
		FT	BASIC_FIBROBLAST_GROWTH_FACTOR_RECEPTOR 1	
		FT	EXTRACELLULAR (POTENTIAL).	
		FT	CYTOSOLIC (POTENTIAL).	
		FT	PROTEIN_KINASE.	
		FT	IG-LIKE C2-TYPE 1.	
		FT	IG-LIKE C2-TYPE 2.	
		FT	IG-LIKE C2-TYPE 3.	
		FT	ASP/GLU-RICH (HIGHLY ACIDIC).	
		FT	PROTEIN_KINASE.	
		FT	ATP (BY SIMILARITY).	
		FT	ATP (BY SIMILARITY).	
		FT	ATP (BY SIMILARITY).	
		FT	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).	
		FT	POTENTIAL.	
		FT	POTENTIAL.	
		FT	POTENTIAL.	
		FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschuler S.F., Zeeberg K.H., Buetow K.H., Moore T., Max S.I., Wang J.J., Bhat N.K., Hopkins R.F., Jordan H., Rubin G.M., Heieh P., Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEvani P.J., McKernan J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [13]

RN MUTAGENESIS OF TYR-766. RX MEDLINE=92357144; PubMed=1379697;

RA Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J., del Rosario M., Mirda D., Williams L.T., Spivak T., Honegger A.M., Mohammadi M., Dionne C.A., Li W., Lin N., Spivak T., Honegger A.M., Jaye M., Schlessinger J., "Point mutation of an FGF receptor abolishes phosphatidylinositol turnover and Ca²⁺ flux but not mitogenesis.", Nature 358:678-681 (1992). [14]

RN MUTAGENESIS OF TYR-766. RX MEDLINE=92357145; PubMed=1379698;

RA Mohammadi M., Mirda D., Williams L.T., Spivak T., Honegger A.M., Jaye M., Schlessinger J., "Point mutation in FGF receptor eliminates phosphatidylinositol hydrolysis without affecting mitogenesis.", Nature 358:681-684 (1992). [15]

RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 464-762. RX MEDLINE=96361355; PubMed=8752212;

RA Mohammadi M., Schlessinger J., Hubbard S.R.; RT autoinhibitory mechanism.; Cell 86:577-587(1996). [16]

RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 464-762. RX MEDLINE=97284786; PubMed=139660;

RA Mohammadi M., McMahon G., Sun L., Tang C., Hirth P., Yeh B.K., Pulley L.J., Schlessinger J., "Structures of the tyrosine kinase domain of fibroblast growth factor receptor in complex with inhibitors.", Science 276:955-960(1997). [17]

RN VARIANT PS ARG-252. RX MEDLINE=95179173; PubMed=7874169;

RA Muenke M., Scheil U., Hehr A., Robin N.H., Losken H.W., Schinzel A., Pulley L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.; RT "A common mutation in the fibroblast growth factor receptor 1 gene in Pfeiffer syndrome."; Nat. Genet. 8:269-274 (1994).

CC -!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter form of the receptor could be a receptor for acidic FGF (aFGF). CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + Protein tyrosine phosphate.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event: Alternative splicing; Named isoforms=7; Comment: Additional isoforms seem to exist; Name=Alpha A1; Isoid=P11362-1; Sequence=Displayed; Name=Alpha B1;

CC Isoid=P11362-2; Sequence=VSP_002960; Name=Beta A1; Isoid=P11362-3; Sequence=VSP_002958; Name=Beta B1;

CC Isoid=P11362-4; Sequence=VSP_002958; VSP_002960; Name=Gamma A1; Isoid=P11362-5; Sequence=VSP_002957;

CC Isoid=P11362-6; Sequence=VSP_002960; Name=Gamma B1;

CC Isoid=P11362-7; Sequence=VSP_002959; Name=A1; Isoid=P11362-8; Sequence=VSP_002961; DISEASE: Defects in Pfeiffer syndrome (25). [NM_1016001], also known as acrocephalosynostosis (premature type V (ACSS5)). PS is characterized by craniosynostosis (enlargement of the skull sutures) with deviation and enlargement of the thumbs and great toes, brachymetaphyseal, with phalangeal ankylosis and a varying degree of soft tissue syndactyly.

CC -!- DISEASE: Involved in a t(8;13)(p12;q12) chromosomal translocation which involves EGFR and ZNF198. The resulting transcript is a possible candidate for stem cell leukemia lymphoma syndrome/SCLL.

CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.

CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/chromancer/Genes/FGFR1113.html".

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Query Match Score 19.3%; Best Local Similarity 30.2%; Matches 97; Conservative 30%; Pred. No. 7.2e-25; Indels 67; Mismatches 127; Gaps 5;

Qy 100 TPALA-----KLYQVBPREQ--LSEVILEQICSGSCGPFRAMMNTGDPSKPKSVIL 146 Db 454 TPMLAGTYSEYLPPDPRWELDRLVLGKPJEGCGQVILAEAGLDKDNRVTKVAV 513

Qy 147 KALKPAGLHEVQDFGLRIQPHQVIGKHNLYVOLBGCCTEKPLIYMLVEDYAQGDLIGFL 206 Db 514 KMLKSDATEKDLSLISEMEMKMKHKNINLIGACTQGPLYIVTEASKGNREYL 573

Qy 207 WTCCRQDWMTMDGLY-----DLTERQVYHIGKQVILALEFTQERHLFHGDVAARN 256 Db 574 QARR----PFGLEYCYNPSHNPPEQCLSSRDLVSCPAQVARGMEYLASKCIRHDIAARN 628

Qy 257 ILMQSQTAKLGLGIALEYTRGAISSST--IPLKWLAPERLILRPASTRADWSFGI 314 Db 629 VLVTENDVMKTADEFGIARDIHIDYXKKTTNGRLPKWKWPAEALFDIYTHQSDWSFGV 688

Qy 315 LLYEMVTLGAPPYPPPTSLLEHLQRKTMKRPSSCTHTMYSIMKSCWRREADRSPR 374 Db 689 LLWETITLGASPyGPVVEELFKLKEGHMDKPSNCINLYMMNRDCWHAVPSORTFK 748

Qy 375 EIRLRLAAIKTADDEAVLV 395 Db 749 QLVEDDRIVALTNSQEYLDL 769

RESULT 11

ABL_MLVAB ID_ABLL_MLVAB STANDARD; PRT; 746 AA. AC P00521; AC DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tyrosine-protein kinase transforming protein ABL (EC 2.7.1.112). GN V-ABL. OS Abelsson murine leukemia virus. OC Viruses; Retroviridae; Mammalian type C retroviruses. OX NCBI_TaxID=1178;

RN [1] RP SEQUENCE FROM N.A. MEDLINE=8321648; PubMed=6304726; RX Reddy E.P., Smith M.J., Srinivasan A.; RT "Nucleotide sequence of Abelsson murine leukemia virus genome:

-!- SUBCELLULAR LOCATION: CYTOPLASMIC; THE MYRISTOYLATED C-ABL PROTEIN
 CC WAS REPORTED TO BE NUCLEAR.
 CC ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=_I;
 CC IsoId=P00520-1; Sequence=Displayed;
 CC Name=_II;
 CC IsoId=P00520-2; Sequence=vsp_004959;
 CC Name=_III;
 CC IsoId=P00520-3; Sequence=vsp_004958;
 CC Name=_IV;
 CC IsoId=P00520-4; Sequence=vsp_004960;
 CC TISSUE SPECIFICITY: Widely expressed.
 CC SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES . ABL
 CC SUBFAMILY:
 -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC
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 or send an email to license@isb-sib.ch).

 DR EMBL; J0395; AAA8241.1; -.
 DR EMBL; U14721; AAB6451.1; -.
 DR EMBL; U14720; AAB6451.1; JOINED.
 DR EMBL; U14721; AAB6450.1; -.
 DR EMBL; U14720; AAB6450.1; JOINED.
 DR EMBL; U14721; AAB6449.1; -.
 DR EMBL; U14721; AAB6448.1; JOINED.
 DR EMBL; U14721; AAB6449.1; -.
 DR EMBL; U14721; AAB6449.1; JOINED.
 DR EMBL; X07539; CAA30411.1; -.
 DR EMBL; X07539; CAA30412.1; -.
 DR EMBL; X07540; CAA30413.1; -.
 DR EMBL; X07541; CAA30414.1; -.
 DR EMBL; M12263; AAA31236.1; -.
 DR EMBL; M12264; AAA3117.1; -.
 DR EMBL; M12265; AAA31138.1; -.
 DR EMBL; M12266; AAA31734.1; -.
 DR EMBL; K03228; AAA31135.1; -.
 DR PDB; 1ABQ; 15-OCT-95.
 DR PDB; 1FFP; 20-SEP-00.
 DR PDB; 1IEP; 01-JUL-03.
 DR PDB; 1M52; 18-SEP-02.
 DR MGD; MGI_87859; Ab11.
 DR GO; GO:000074; P:regulation of cell cycle; IDA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR InterPro; IPR008266; Tyr_Pkinase_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00018; SH2; 1.
 DR PRINTS; PR00404; SHDOMAIN.
 DR PRINTS; PR00442; SH3DOMAIN.
 DR PRINTS; PR00109; TRKINASE.
 DR ProDom; P0000001; Prot_kinase; 1.
 DR ProDom; P0000053; SH2; 1.
 DR ProSite; PS000066; SH3; 1.
 DR ProSite; PS00107; PROTEIN_KINASE_ATP; 1.
 DR ProSite; PS00109; PROTEIN_KINASE_TYR; 1.
 DR ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 KW Phosphorylation; SH2 domain; SH3 domain; Alternative splicing;
 KW Nuclear protein; 3D-structure.

FT DOMAIN 61 121
 FT DOMAIN 127 217
 FT DOMAIN 242 493
 FT DOMAIN 605 609
 FT DOMAIN 18 22
 FT DOMAIN 605 609
 FT DOMAIN 604 1012
 FT DOMAIN 891 897
 FT NP_BIND 248 256
 FT BINDING 271 271
 FT ACT SITE 363 363
 FT MOD_RES 393 393
 FT VARSPLIC 1 26
 FT VARSPLIC 248 256
 FT VARSPLIC 1 26
 FT VARSPLIC 65 68
 FT STRAND 72 72
 FT TURN 77 78
 FT STRAND 79 79
 FT STRAND 82 82
 FT TURN 84 85
 FT STRAND 87 93
 FT TURN 95 96
 FT STRAND 99 104
 FT TURN 105 106
 FT STRAND 107 112
 FT HELIX 113 115
 FT STRAND 116 118
 SQ SEQUENCE 1123 AA; 122676 MW; 284F0830644AFD8F CRC64;

 Query Match 19.1%; Score 419; DB 1; Length 1123;
 Best Local Similarity 34.7%; Pred. No. 2.6e-24;
 Matches 96; Conservative 51; Mismatches 94; Indels 36; Gaps 7;

 Qy 143 SVILKALKEPAGLHEVQDFIGRIQFHQYLGKHNOLVQLEKPLYMLVEDVAQGL 202
 Db 267 TVAVKTLLKEPT-MEVEEFPIKEAAVMKEI-KHPNLUQLGVCPREPFTLTETMYGNL 323
 Qy 203 LGFLWTCRRDVMTMDGLYDLTEKQVHIGQVIALEFQKHLFRGQVDAARNILMQSD 262
 Db 324 LDYLRECNQEVSAVILLYMAT----QISSAMEYLEKQNFHIDLAAARNCLVGEN 374
 Qy 263 LTAKLQGLGLAY---EVYTRGAISSTOTIPLKWLAPERILLRPASTRADVWSFGILLYE 318
 Db 267 TVAVKTLLKEPT-MEVEEFPIKEAAVMKEI-KHPNLUQLGVCPREPFTLTETMYGNL 323
 Qy 375 HLVKVADFGLSRLMTGDTYTAHAGAK---FPIKWTAPESLAYNKFSIKSDVWARFVLLW 431
 Db 432 IATYCNSPGYFDISQVYBLEDYMREREGCPKVKYLMRACQWNNSDRPFAEIHQ 491
 Qy 379 RLEAMK-TADDE-----AVLQVPEL 398
 Db 492 AFETMFQESSISDEVKELGKRGTGGAGSMLOAPEL 528

 RESULT 13
 ABLL HUMAN STANDARD PRT; 1130 AA.
 ID_ABLL HUMAN STANDARD PRT; 1130 AA.
 AC P00519; Q13869; Q13870; Q16133;
 DT 21-JUL-1986 (Rel. 1. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 1. 42, Last annotation update)
 DE Proto-oncogene tyrosine-Protein Kinase ABLI (EC 2.7.1.112) (p150)
 DE (c-ABL).
 GN ABLL OR ABL OR JTK .

- OS Homo sapiens (Human).
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metazoa; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.;
 RC TISSUE-Fibroblast;
 RX MEDLINE=90082420; PubMed=268768;
 RA Einstein E., Einat M., Gokkel E., Marcelle C., Croce C.M., Gale R.P., Canaani E.;
 RT "Nucleotide sequence analysis of human abl and bcr-abl cDNAs.";
 RL Oncogene 4:1477-1481(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=87028219; PubMed=3021337;
 RA Shtrivelman E., Lifshitz B., Gale R.P., Roe B.A., Canaani E.;
 RT "Alternative splicing of RNAs transcribed from the human abl gene and from the bcr-abl fused gene.";
 RL Cell 47:277-284(1986).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS IA AND IB).
 RX TISSUE-Lung carcinoma;
 RX MEDLINE=95394474; PubMed=7665165;
 RA Chissoe S.L., Boenteich A., Wang Y.-F., Wang Y.-P., Burian D., Clifton S.W., Crabtree J., Freeman A., Iyer K., Jian L., Ma Y., McLaury H.-J., Pan H.-Q., Roth S., Wang Z., Zhang G., Heisterkamp N., Groffen J., Roe B.A.,
 RT "Sequence and analysis of the human ABL gene, the BCR gene, and regions involved in the Philadelphia chromosomal translocation.";
 RL Genomics 27:67-82(1995).
 RN [4]
 RP SEQUENCE OF 360-426 FROM N.A.
 RX MEDLINE=83245023; PubMed=6191223;
 RA Groffen J., Heisterkamp N., Reynolds F.H. Jr., Stephenson J.R.,
 RT "Homology between phosphotyrosine acceptor site of human c-abl and viral oncogene products.";
 RT Nature 304:167-169(1983).
 RN [5]
 RP SEQUENCE OF 27-40 FROM N.A.
 RX MEDLINE=88052859; PubMed=2825022;
 RA Einstein E., Marcelle C., Rosner A., Canaani E., Gale R.P., Drezen O., Smith S.D., Croce C.M.;
 RT "A new fused transcript in Philadelphia chromosome positive acute
 RT lymphocytic leukaemia";
 RL Nature 330:386-388(1987).
 RN [6]
 RP SEQUENCE OF 825-845 FROM N.A.
 RX MEDLINE=94142331; PubMed=7545908;
 RA Inokuchi K., Futaki M., Dan K., Nomura T.;
 RT "Sequence analysis of the mutation at codon 834 and the sequence variation of codon 837 of c-abl gene.";
 RL Leukemia 8:343-344(1994).
 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=92727068; PubMed=1505033;
 RA Overdin M., Rios C.B., Mayer B.J., Baltimore D., Cowburn D.;
 RT "Three-dimensional solution structure of the src homology 2 domain of c-abl.";
 RL Cell 70:697-704(1992).
 RN [8]
 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=93101588; PubMed=1281542;
 RA Overdin M., Mayer B.-J., Rios C.B., Baltimore D., Cowburn D.;
 RT "Secondary structure of Src homology 2 domain of c-Ab1 by heteronuclear NMR spectroscopy in solution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11673-11677(1992).
 RP STRUCTURE BY NMR OF SH3 DOMAIN.
 RX MEDLINE=96131878; PubMed=1590002;
 RA Gossen Y.Q., Zheng J., Overduin M., Mayer B.J., Cowburn D.;
 RT "The solution structure of Ab1 SH3, and its relationship to SH2 in the SH1(32) construct.";
 RT Structure 3:1075-1086(1995).
- RN [10] 3D-STRUCTURE MODELING OF SH3 DOMAIN.
 RP RX MEDLINE=95199229; PubMed=7892170;
 RX RA Pisabarro M.T., Ortiz A.R., Serrano L., Wade R.C.;
 RT "Homology modeling of the Ab1-SH3 domain.";
 RL Proteins 20:203-215(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 57-218.
 RX MEDLINE=96398698; PubMed=9805556;
 RA Nam H.-J., Haser W.G., Roberts T.M., Frederick C.A.;
 RT "Intramolecular interactions of the regulatory domains of the Bcr-Abl kinase reveal a novel control mechanism.";
 RL Structure 4:1105-1114(1996).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 64-121.
 RX MEDLINE=98365516; PubMed=9698566;
 RA RA Pisabarro M.T., Serrano L., Wilmanns M.;
 RT "Crystal structure of the Ab1-SH3 domain complexed with a designed high affinity peptide ligand: implications for SH3-ligand interactions.";
 RL Structure 5:1115-1124(1998).
 RN [13]
 RP STRUCTURE BY NMR OF 62-122 IN COMPLEX WITH CRK.
 RX MEDLINE=22294994; PubMed=12384776;
 RA Donaldson L.W., Gish G., Pawson T., Kay L.E., Forman-Kay J.D.;
 RT "Structure of a regulatory complex involving the Ab1 SH3 domain, the Crk SH2 domain, and a Crk-derived phosphopeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14053-14058(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=IA;
 CC IsoId=P00519-1; Sequence=Displayed;
 CC Name=IB;
 CC IsoId=P00519-2; Sequence=VSP_004957;
 CC -!- TISSUE SPECIFICITY: Widely expressed;
 CC -!- DISEASE: Participates in a t(9;22) (q34;q11) chromosomal translocation that produces a BCR-ABL oncogene responsible for chronic myeloid leukemia (CML), acute myeloid leukemia (AML) and acute lymphoblastic leukemia (ALL).
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infoflobiogen.fr/services/chromcancer/Genes/ABL.html".
 CC ---
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 CC ---
 DR EMBL; X16416; CAA3438.1;-.
 DR EMBL; M14752; AAA51561.1;-.
 DR EMBL; U07563; AAB60394.1;-.
 DR EMBL; U07563; AAB60393.1;-.
 DR EMBL; U07561; AAB60393.1;-.
 DR EMBL; S69223; AD14034.1;-.
 DR PIR; S08519; TIRUA.
 DR PDB; 1AB2; 31-TIAN-94.
 DR PDB; 2ABL; 04-SEP-97.
 DR PDB; 1AWO; 28-JAN-98.
 DR PDB; 1BBZ; 25-NOV-98.
 DR PDB; 1ABL; 01-NOV-94.
 DR PDB; 1IJU; 06-NOV-02.
 DR Genew; HGNC:76; ABL1.
 DR MIM; 189980;-.
 GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.

DR	GO; GO:0006298; P:DNA damage response; signal transduction re... ; TAS.
DR	GO; GO:0000074; P:mismatch repair; TAS.
DR	GO; GO:0006355; P:regulation of cell cycle; TAS.
DR	GO; GO:0000115; P:specific transcription in mitotic cell cycle; TAS.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR000980; SH2.
DR	InterPro; IPR001452; SH3.
DR	InterPro; IPR001245; Tyr_Pkinase.
DR	InterPro; IPR008266; Tyr_Pkinase_AS.
DR	Pfam; PF00069; kinase; 1.
DR	Pfam; PF00017; SH2; 1.
DR	Pfam; PF0001; SH3; 1.
DR	PRINTS; PRO0401; SH2DOMAIN.
DR	PRINTS; PRO0452; SH2DOMAIN.
DR	PRINTS; PRO109; TIRKINASE.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	ProDom; PD000093; SH2; 1.
DR	ProDom; PD000066; SH3; 1.
DR	SMART; SM00052; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00119; TyrK; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS50002; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS50001; SH2; 1.
DR	PROSITE; PS50002; SH3; 1.
KW	Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding; Phosphorylation; SH2 domain; SH3 domain; Chromosomal translocation; 3D-structure; Alternative splicing.
PT DOMAIN	61 121
FT DOMAIN	127 217
FT DOMAIN	242 493
FT DOMAIN	605 609
FT DOMAIN	18 22
FT DOMAIN	605 609
FT DOMAIN	782 1019
FT DOMAIN	897 903
FT SITE	26 27
NP BINDING	248 256
FT BINDING	271 271
ACT SITE	363 363
MOD RES	393 393
VARSPLIC	1 26
FT	
Query Match	19.0%; Score 417; DB 1; Length 1130;
Best Local Similarity	34.7%; Pred. No. 3.8e-24;
Matches	96; Conservative 49; Mismatches 96; Indels 36; Gaps 7
Qy	143 SVI KALKEAGLILHEQDFIGRIQPHQYLGKXHNRIVQLBGCCTKLPLVNLVDEAQGDL 2038
Ddb	267 TVAKT KLKEPTD-MEVETEAVMKEI-KHPNIVQLGVCTPEPPFYITPBMTRYGNL 3224
Qy	203 LGF WTCRRDVMTMDGLYLDTEKQVHICKQVLALEFQQLFLHGDXAARNILMQSD 2624
Ddb	324 LDYRECNEQEVNAVLLIMAT-----QISSAMELEKKNFIRHDAA RCVLG EN 374
Qy	263 LTA KLQGLIAY-----EVYTRGAISSTQTIPKLKIAPELILRASISTRADWSSGILYE 318
Ddb	375 HLVVA DFGSLRLMTGDTTAHAZAK--FPIKTTAPESTLAYNFSIKSDVWARTGVLLME 4311
Qy	319 MVT GAPPVEPVPSLILEHLQRKXIMKRSSCHTMYSIMKSQWRWREADRPPRERL 378
Ddb	432 IAT QMSPPQSVYELQKDYMREREGCDEVYILMPCQWNFSDRPSPAEHQ 4911
Qy	379 RLEAAIK-TADDE-----AVLOVPEL 398
Ddb	492 A FETMFQESSIDVEKELGKQGVRAVASTLQAPL 528

FRG1	XENLA	STANDARD;	PRT;	812 AA.
ID	FRGL_XENLA			
AC	P22182;			
DT	01-AUG-1991 (Rel. 1.9, Created)			
DT	01-AUG-1991 (Rel. 1.9, Last sequence update)			
DT	10-OCT-2003 (Rel. 2.12, Last annotation update)			
DE	Fibroblast growth factor receptor 1 precursor (EC 2.7.1.112).			
GN	EGFR-1.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopoda; Xenopus.			
OC	NCBI_TaxID=3355;			
OX				
RN				
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=91045998; PubMed=2172985;			
RA	Musci T.J., Amaya E., Kirshchner M.W.;			
RT	"Regulation of the fibroblast growth factor receptor in early Xenopus embryos."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8365-8369 (1990)			
CC	-!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.			
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.			
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements.html or send an email to license@isb-sib.ch).			
CC	DR EMBL; U24491; AAA86368.1; -.			
DR	PTR; A36477; A36477.			
DR	HSSP; P11362; IEGK.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003598; Ig_c2.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR001245; Tyr_Pkinase.			
DR	InterPro; IPR008266; Tyr_Pkinase_AS.			
DR	PFam; PF00069; pkinkse; 1.			
DR	PRINTS; PRO0109; TYRKINASE.			
DR	SMART; SM00408; IgC2; 3.			
DR	SMART; SM00219; Tyrfc; 1.			
DR	PROSITE; PS50835; IG_LIKE; 3.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TIR; 1.			
KW	Receptor; Glycoprotein; Tyrosine-Protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain; Repeat; Signal.			
KW	Peptidase; Signal.			
FT	SIGNAL	1	20	BY SIMILARITY.
FT	CHAIN	21	812	FIBROBLAST GROWTH FACTOR RECEPTOR 1.
FT	DOMAIN	21	371	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	372	393	POTENTIAL.
FT	DOMAIN	394	812	CYTOSPLASMIC (POTENTIAL).
FT	DOMAIN	33	110	IG-LIKE C2-TYPE 1.
FT	DOMAIN	154	242	IG-LIKE C2-TYPE 2.
FT	DOMAIN	251	353	IG-LIKE C2-TYPE 3.
FT	DOMAIN	472	761	PROTEIN KINASE.
FT	NP_BIND	478	486	ATP (BY SIMILARITY).
FT	BINDING	508	508	ATP (BY SIMILARITY).
FT	ACT_SITE	617	617	BY SIMILARITY.
FT	MOD_RES	648	648	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	76	76	N-LINKED (GLCNAC). (POTENTIAL).
FT	CARBOHYD	116	116	N-LINKED (GLCNAC). (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC). (POTENTIAL).

FT	CARBOHYD	177	177	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	236	236	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	313	313	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	326	326	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	812 AA;	90502 MW;	B06333 BAFFAC5C9B CRC64;	
SEQUENCE					
Query Match		19.0%	Score 416; DB 1; Length 812;		
Best Local Similarity	29.7%	Pred. 2..9e-22;			
Matches	97;	Conservative	Mismatches 137; Indels 26; Gaps 5;		
Qy	92 VENFLGANTPAKL-----OPREO--LSEVLEQICSGSCCPFRANNTGDP	138			
Db	440 VRLSSSQTPLMSGLSEYELPEDPRWVEARDLILGKPLGEFCFGVYMAEIGLDKEKP	499			
Qy	139 SKPKSVLKALKEPAGLIEEVQDFLGRICFHQYLGKHKNLVQLEGCCTEKLPLMVLVEDA	198			
Db	500 NKVTKVAKMLKSDASEKDSLISEMEMMMKMGKHKNLNILGACTDGPLVIVVETYS	559			
Qy	199 QCDLIGFWT-----CRRDWMTMPCGLLYDLTEKQWYHICKQVYLAEFQEKHLFG	250			
Db	560 KGNLREYLRARRPAPMEYCYNPNTPCVPDOL---LSFKDOLVSCAYQVARGMDYLASKRCIHR	616			
Qy	251 DVARNILIMQSDLTAKEGLGLAYEVTRGAISSTQT-IPWKWLADERLLRPARSIAD	308			
Db	617 DLAARNVLYTEDNIMKIADEGLARDIHHIDYKKTNGRLPVKWMAPALFRIYTHQSD	676			
Qy	309 VNSFGILLYEMYTGLAPPYPEVPTSTILEHLQRKTMKRPSSTHTMYSIMSKCWRAREA	368			
Db	677 VNSFGVLWEIFLFGGSYPGVMEELFKLKEGHMRMKPTINTNLYMMKDCWHAmps	736			
Qy	369 DRSPRETRLRFAAIKTAIKDDEAVLQV	395			
Db	737 QRPENQIVEDLRLAISNQEYLDL	763			
RESUL T 15					
FOR1_RAT	STANDARD;	PRT;	822 AA.		
ID	FOR1_RAT				
AC	Q04589;				
DT	01-JUN-1994	(Rel 29, Created)			
DT	01-JUN-1994	(Rel 29, Last sequence update)			
DT	10-OCT-2003	(Rel 42, Last annotation update)			
DE	Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)				
DE	(IGFR-1) (bFGF-R) (MFR).				
GN	FGFR1 or FGFR.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TAXID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MBELINE:76824; PubMed:8382532;				
RT	Yazaki N., Hiroko F., Mitsuhiro O., Toshiyuki K., Nobuyuki I.; "The structure and expression of the FGF receptor-1 mRNA isoforms in rat tissues"; Biochim. Biophys. Acta 1172:37-42 (1993).				
CC	-!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter form of the receptor could be a receptor for acidic FGF (aFGF).				
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- SIMILARITY: Belongs to the fibroblast growth factor receptor family.				
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	CC	CC	CC	CC	CC
CC	DR	DR	DR	DR	DR
CC	EMBL; D12438; BAA02059.1; -.	S2840.	HSSP; P11362; 1PGK.	InterPro; IPR007110; Ig-like.	InterPro; IPR003598; Ig c2.
CC	DR	DR	DR	DR	DR
CC	InterPro; IPR00719; Prot kinase.	InterPro; IPR001245; Tyr_P kinase.	InterPro; IPR003266; Tyr_P kinase_AS.	InterPro; IPR00047; ig; 3.	InterPro; IPR00069; kinase; 1.
CC	DR	DR	DR	DR	DR
CC	SMART; SM00408; IgC2; 3.	SMART; SM00219; TyrKc; 1.	PROSITE; PS00835; Ig_LIKE; 3.	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	PROSITE; PS05011; PROTEIN_KINASE_DOM; 1.
CC	DR	DR	DR	DR	DR
CC	PROSITE; PS0109; PROTEIN_KINASE_TYR; 1.	KW	KW	KW	KW
CC	Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; TransFerase; Phosphorylation; Transmembrane; Signal;	Immunoglobulin domain; Repeat; POTENTIAL.	Protein kinase; Tyrosine-phosphorylation; Transmembrane; Signal; POTENTIAL.	ATP (BY SIMILARITY).	ATP (BY SIMILARITY).
CC	FT	FT	FT	FT	FT
CC	SIGNAL	1	21	21	21
CC	CHAIN	22	822	822	822
CC	FT	FT	FT	FT	FT
CC	EXTRACELLULAR	POTENTIAL.	POTENTIAL.	POTENTIAL.	POTENTIAL.
CC	FT	FT	FT	FT	FT
CC	TRANSMEM	376	397	397	397
CC	DOMAIN	398	822	822	822
CC	FT	FT	FT	FT	FT
CC	DOMAIN	25	119	119	119
CC	FT	FT	FT	FT	FT
CC	DOMAIN	158	246	246	246
CC	FT	FT	FT	FT	FT
CC	DOMAIN	255	357	357	357
CC	FT	FT	FT	FT	FT
CC	NP_BIND	478	767	767	767
CC	FT	FT	FT	FT	FT
CC	BINDING	514	514	514	514
CC	FT	FT	FT	FT	FT
CC	ACT_SITE	623	623	623	623
CC	FT	FT	FT	FT	FT
CC	MOD_RES	654	654	654	654
CC	DISULFID	55	101	101	101
CC	FT	FT	FT	FT	FT
CC	DISULFID	178	230	230	230
CC	FT	FT	FT	FT	FT
CC	DISULFID	277	341	341	341
CC	FT	FT	FT	FT	FT
CC	CARBOHYD	77	77	77	77
CC	FT	FT	FT	FT	FT
CC	CARBOHYD	117	117	117	117
CC	FT	FT	FT	FT	FT
CC	CARBOHYD	227	227	227	227
CC	FT	FT	FT	FT	FT
CC	CARBOHYD	240	240	240	240
CC	FT	FT	FT	FT	FT
CC	CARBOHYD	264	296	296	296
CC	FT	FT	FT	FT	FT
CC	CARBOHYD	317	317	317	317
CC	FT	FT	FT	FT	FT
CC	SEQUENCE	330	330	330	330
CC	822 AA;	91824 MW;	E59D24D0A1DE5C5	CRC64;	
CC	Query	18.9%	Score 415; DB 1; Length 822;		
CC	Best Local Similarity	29.9%	Pred. No. 3.6e-24;		
CC	Matches	96;	Conservative	67; Mismatches	128; Indels 30; Gaps 5;
CC	TPALA-----KQVPRREQ-----LSEVLEQICSGSCGP1FRANNTGDPSPKPSVYL	146			
CC	DB	454 TPMLAGSYEYLPDPRVLPRLVGRPLGCFGVVLAEAGLQDKPAPRVTKVA	513		
CC	QY	147 KALEKPAGLHEVDLGIQPHQYLGKHNVLVOLBGCTEKLPLMYMLEDVAQDGLGFL	206		
CC	DB	514 KMILKSDATEKDLSDLISEMEMMMKIGKHNLTINLGACTQDGLYVIVEYASRKNLREYL	573		
CC	QY	207 WTCRDVNTMDGLY-----DLTEKQVHIGCQVLLAEFLQPKHNGDVARN	256		
CC	DB	574 QARR-----PPGLEYCYNPSHNPBEQLSSKDLVSCATQVARGMEYLASKKCITHDLAARN	628		
CC	QY	257 ILMOSDILTAKLCGSGLATEVYTRGAISSTQT-----PLKWLAPBLRLLPASIRADVWSFGI	314		
CC	DB	629 VLTEDNWKIAFGLDIAHHDYKETTNGLPVTKMAPAELDPRYTHQSDWMSGV	688		
CC	QY	315 LIYEMVTLGAPPYEVPPPTSILHQLREKTMKRPSSTHTMYSIMKSCWRMREADRSPR	374		

Db 689 LLWEIFTLGGSPNPGVPVEELPKLLKEGHMDKPSNCTNLYMMRDCTWNAVPSQRPTFK 748
Qy 375 ELRLRLEAAIKPADDEAVLQV 395
Db :|: |: |: |:
749 QLVEDLDRIVALTTSNOEYLDL 769

Search completed: June 14, 2004, 18:44:46
Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:42:14 ; Search time 20 Seconds
 (without alignments)
 2029.641 Million cell updates/sec

Title: US-10-040-884-3
 Perfect score: 2192
 Sequence: 1 MGMTMILECSLSDKLCVIQ.....LYAAVAGIRVESLFYNYSML 422

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2192	100.0	422	T48680 hypothetical prote
2	465.5	21.2	829	JC4583 fibroblast growth
3	459.5	21.0	818	JC4058 fibroblast growth
4	455.5	20.8	822	S19947 fibroblast growth
5	455.5	20.8	822	B49151 fibroblast growth
6	453.5	20.7	800	TWHU2F fibroblast growth
7	453.5	20.7	800	A4891 heparin-binding gr
8	447	20.4	797	S28579 fibroblast growth
9	446.5	20.4	806	protein-tyrosine k
10	444	20.3	801	155963 fibroblast growth
11	444	20.3	806	1 TVHF3 fibroblast growth
12	439.5	20.1	713	150128 heparin-binding gr
13	434	19.8	802	1 TVHF4 fibroblast growth
14	433	19.8	705	2 S51635 fibroblast growth
15	433	19.8	707	2 A38429 keratinocyte grow
16	433	19.8	820	2 S17295 fibroblast growth
17	433	19.8	821	1 TWBSK fibroblast growth
18	432	19.7	682	2 A35969 heparin-binding gr
19	432	19.7	733	2 T49293 fibroblast growth
20	432	19.7	822	2 A4889 fibroblast growth
21	431	19.7	799	2 S18209 fibroblast growth
22	430	19.6	707	2 A54846 fibroblast growth
23	430	19.6	729	2 A56745 fibroblast growth
24	430	19.6	822	2 B56846 fibroblast growth
25	427.5	19.5	822	1 TVNSFG fibroblast growth
26	427	19.5	821	1 TVHF2 fibroblast growth
27	427	19.5	822	2 A44081 fibroblast growth
28	426	19.4	822	2 A41794 fibroblast growth
29	424.5	19.4	832	2 JH0932 fibroblast growth

330	424	19.3	819	1	TVCHFG	fibroblast growth
331	424	19.3	822	1	TVHDFG	fibroblast growth
332	423	19.3	769	2	S16236	fibroblast growth
333	423	19.3	814	1	A39752	fibroblast growth
334	421	19.2	650	1	JC1450	fibroblast growth
335	419	19.1	981	1	ROMGM	Gag-Ab1 polyprotei
336	419	19.1	1123	2	A39962	kinase-related tra
337	418	19.1	824	2	S36439	fibroblast growth
338	417	19.0	415	2	I65223	heparin-binding fi
339	417	19.0	1130	1	TVHUA	protein-tyrosine k
340	416	19.0	812	1	A36477	fibroblast growth
341	415	18.9	748	2	S41050	fibroblast growth
342	415	18.9	750	2	S41051	fibroblast growth
343	415	18.9	822	2	S29840	fibroblast growth
344	415	18.9	823	2	B35963	protein-tyrosine k
345	412	18.8	824	2	S24108	protein-tyrosine k

ALIGNMENTS

RESULT 1
T48680 hypothetical protein DKRZP761P1010.1 - human
C;Species: *Homo sapiens* (man)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48680
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
Submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24433

A;Accession: T48680
 A;Stratus: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-422 <AAA>
 A;Cross-references: EMBL:AI353940
 A;Experimental source: adult amygdala; clone DKFZp761P1010
 C;Genetics:
 D;Notes: Drosophila melanogaster

Query Match	Score	DB	Length
Best Local Similarity	100.0%	DB 2;	Length 422;
Matches 422;	Pred. No. 6.2e-103;	Mismatches 0;	Indels 0;
Qy	1	MGMTRMILKCSLSKLCVIQEKQYEVILVPTPLTVTFLILLGVTLWLFIREOPTQQRSQ	60
Db	1	MGMTRMILKCSLSKLCVIQEKQYEVILVPTPLTVTFLILLGVTLWLFIREOPTQQRSQ	60
Qy	61	PQGIAVPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPLAKLQVPREQUSLEQI	120
Db	61	PQGIAVPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPLAKLQVPREQUSLEQI	120
Qy	121	CSGSGPPIRANNTGDPSPKPSVTKALKAKEPLAHLPEVDFLGRIQFFQYQLGRKHNLVQL	180
Db	121	CSGSGPPIRANNTGDPSPKPSVTKALKAKEPLAHLPEVDFLGRIQFFQYQLGRKHNLVQL	180
Qy	181	EGCCTEKPLMVLVEDVAQGDLGLCFWLTCRRDWTMGLYDLTEKVQTHIGKQVLLALE	240
Db	181	EGCCTEKPLMVLVEDVAQGDLGLCFWLTCRRDWTMGLYDLTEKVQTHIGKQVLLALE	240
Qy	241	FLOQBHLFHGDAARNTIMQSDLTAKLCGJGLAYEVTRGAISSTQTPLKMLAPERLL	300
Db	241	FLOQBHLFHGDAARNTIMQSDLTAKLCGJGLAYEVTRGAISSTQTPLKMLAPERLL	300
Qy	301	RPASRADWSFGILLYEMVTLGAPPYPPVPPSISLHLQRKXIMKRPESSCTHTMYSIMK	360
Db	301	RPASRADWSFGILLYEMVTLGAPPYPPVPPSISLHLQRKXIMKRPESSCTHTMYSIMK	360
Qy	361	SCWRREADRSPSPRLURLEAAIKTADDEAVLQPELYAVGIRVESLFYNYS	420
Db	361	SCWRREADRSPSPRLURLEAAIKTADDEAVLQPELYAVGIRVESLFYNYS	420
Qy	421	ML	422

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	2192	100.0	422	2	T48680		hypothetical prote
2	465.5	21.2	829	2	JC4583		fibroblast growth
3	459.5	21.0	818	2	JC4058		fibroblast growth
4	455.5	20.8	822	2	S1947		fibroblast growth
5	455.5	20.8	822	2	B49151		fibroblast growth
6	453.5	20.7	800	1	TVHUF2P		fibroblast growth
7	453.5	20.7	800	2	A48391		heparin-binding gr
8	447	20.4	797	2	S38579		fibroblast growth
9	446.5	20.4	806	2	A35963		protein-tyrosine k
10	444	20.3	801	2	I55363		fibroblast growth
11	444	20.3	806	1	TVHFU3		fibroblast growth
12	439.5	20.1	713	2	I50128		fibroblast growth
13	434	19.8	802	1	TVHUF4		fibroblast growth
14	433	19.8	705	2	S51635		fibroblast growth
15		19.8	707	2	A38429		keratinocyte growt
16	433	19.8	820	2	S17395		fibroblast growth
17	433	19.8	821	1	TVMSBK		fibroblast growth
18	432	19.7	682	2	A35969		heparin-binding gr
19	432	19.7	733	2	I49293		fibroblast growth
20	432	19.7	822	2	I49289		fibroblast growth
21	431	19.7	799	2	S18209		fibroblast growth
22	430	19.6	707	2	A54846		fibroblast growth
23	430	19.6	729	2	A56795		fibroblast growth
24	430	19.6	822	2	B54846		fibroblast growth
25	427.5	19.5	822	1	TVMSFG		fibroblast growth
26	427	19.5	821	1	TVHUF2		fibroblast growth
27	426	19.5	822	2	A45081		keratinocyte growt
28	426	19.4	822	2	A41794		keratinocyte growt
29	424.5	19.4	832	2	JH0193		fibroblast growth

Db 421 ML 422

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

RESULT 2

JC4583

fibroblast growth factor receptor 4B precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 16-Jul-1999

C;Accession: JC4583

R'Aiou, J.F.; Clavillier, L.; Boucaut, J.C.

Biochim. Biophys. Res. Commun. 218, 198-204, 1996

A;Title: Early regional expression of a novel Xenopus fibroblast growth factor receptor

A;Reference number: JC4583 ; MUID: 96136300 ; PMID: 8571131

A;Molecule type: mRNA

A;Residues: 1-818 <SHT>

A;Cross-references: DDBJ:D31761; NID:9809527; PID:BA006539.1; PID:9809528

A;Genetics:

A;Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 428/1; 556/1; 619/1; 6

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein

C;Keywords: ATP; growth factor receptor; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-818/Domain: fibroblast growth factor receptor 4 #status predicted <SIG>

F:56-110/Domain: immunoglobulin homology <IM1>

F:132-137/Domain: acidic #status predicted <AD1>

F:177-238/Domain: immunoglobulin homology <IM2>

F:276-347/Domain: immunoglobulin homology <IM3>

F:382-402/Domain: transmembrane #status Predicted <TMM>

F:487-504/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-816 <SHT>

A;Cross-references: EMBL:X65059

C;Species: Xenopus laevis (African clawed frog)

C;Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000

C;Accession: JC4058

R;Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiokawa, K.

Gene 152, 215-219, 1995

A;Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor

A;Reference number: S19947

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-802 <SHT>

A;Cross-references: EMBL:X65059

C;Superfamily: basic fibroblast growth factor receptor

C;Keywords: ATP; growth factor receptor

F:354/Domain: immunoglobulin homology <IM1>

F:484-769/Domain: protein kinase homology <KIN>

F:492-500/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-818 <SHT>

A;Cross-references: DDBJ:D31761; NID:9809527; PID:BA006539.1; PID:9809528

A;Genetics:

A;Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 428/1; 556/1; 619/1; 6

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein

C;Keywords: ATP; growth factor receptor; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

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F:276-347/Domain: immunoglobulin homology <IM3>

F:382-402/Domain: transmembrane #status Predicted <TMM>

F:487-504/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-816 <SHT>

A;Cross-references: EMBL:X65059

C;Species: Xenopus laevis (African clawed frog)

C;Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000

C;Accession: JC4058

R;Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiokawa, K.

Gene 152, 215-219, 1995

A;Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor

A;Reference number: S19947

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-802 <SHT>

A;Cross-references: EMBL:X65059

C;Superfamily: basic fibroblast growth factor receptor

C;Keywords: ATP; growth factor receptor

F:354/Domain: immunoglobulin homology <IM1>

F:484-769/Domain: protein kinase homology <KIN>

F:492-500/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-818 <SHT>

A;Cross-references: DDBJ:D31761; NID:9809527; PID:BA006539.1; PID:9809528

A;Genetics:

A;Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 428/1; 556/1; 619/1; 6

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein

C;Keywords: ATP; growth factor receptor; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-818/Domain: fibroblast growth factor receptor 4 #status predicted <SIG>

F:56-110/Domain: immunoglobulin homology <IM1>

F:132-137/Domain: acidic #status predicted <AD1>

F:177-238/Domain: immunoglobulin homology <IM2>

F:276-347/Domain: immunoglobulin homology <IM3>

F:382-402/Domain: transmembrane #status Predicted <TMM>

F:487-504/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-816 <SHT>

A;Cross-references: EMBL:X65059

C;Species: Xenopus laevis (African clawed frog)

C;Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000

C;Accession: JC4058

R;Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiokawa, K.

Gene 152, 215-219, 1995

A;Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor

A;Reference number: S19947

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-802 <SHT>

A;Cross-references: EMBL:X65059

C;Superfamily: basic fibroblast growth factor receptor

C;Keywords: ATP; growth factor receptor

F:354/Domain: immunoglobulin homology <IM1>

F:484-769/Domain: protein kinase homology <KIN>

F:492-500/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-818 <SHT>

A;Cross-references: DDBJ:D31761; NID:9809527; PID:BA006539.1; PID:9809528

A;Genetics:

A;Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 428/1; 556/1; 619/1; 6

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein

C;Keywords: ATP; growth factor receptor; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-818/Domain: fibroblast growth factor receptor 4 #status predicted <SIG>

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F:132-137/Domain: acidic #status predicted <AD1>

F:177-238/Domain: immunoglobulin homology <IM2>

F:276-347/Domain: immunoglobulin homology <IM3>

F:382-402/Domain: transmembrane #status Predicted <TMM>

F:487-504/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-816 <SHT>

A;Cross-references: EMBL:X65059

C;Species: Pleurodeles waltlii (Iberian ribbed newt)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995

R;Shi, D.L.; Peige, J.J.; DeSimone, D.W.; Boucaut, J.C.

A;Description: Receptors during early development of the urodele Pleurodeles waltlii.

A;Reference number: S19947

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-802 <SHT>

A;Cross-references: EMBL:X65059

C;Superfamily: basic fibroblast growth factor receptor

C;Keywords: ATP; growth factor receptor

F:354/Domain: immunoglobulin homology <IM1>

F:484-769/Domain: protein kinase homology <KIN>

F:492-500/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-818 <SHT>

A;Cross-references: DDBJ:D31761; NID:9809527; PID:BA006539.1; PID:9809528

A;Genetics:

A;Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 428/1; 556/1; 619/1; 6

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein

C;Keywords: ATP; growth factor receptor; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-818/Domain: fibroblast growth factor receptor 4 #status predicted <SIG>

F:56-110/Domain: immunoglobulin homology <IM1>

F:132-137/Domain: acidic #status predicted <AD1>

F:177-238/Domain: immunoglobulin homology <IM2>

F:276-347/Domain: immunoglobulin homology <IM3>

F:382-402/Domain: transmembrane #status Predicted <TMM>

F:487-504/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-816 <SHT>

A;Cross-references: EMBL:X65059

C;Species: Xenopus laevis (African clawed frog)

C;Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000

R;Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiokawa, K.

Gene 152, 215-219, 1995

A;Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor

A;Reference number: S19947

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-802 <SHT>

A;Cross-references: EMBL:X65059

C;Superfamily: basic fibroblast growth factor receptor

C;Keywords: ATP; growth factor receptor

F:354/Domain: immunoglobulin homology <IM1>

F:484-769/Domain: protein kinase homology <KIN>

F:492-500/Region: protein kinase ATP-binding motif

A;Reference number: JC4058 ; MUID: 95137391 ; PMID: 7835703

A;Molecule type: mRNA

A;Residues: 1-818 <SHT>

A;Cross-references: DDBJ:D31761; NID:9809527; PID:BA006539.1; PID:9809528

A;Genetics:

A;Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 428/1; 556/1; 619/1; 6

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein

C;Keywords: ATP; growth factor receptor; transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-818/Domain: fibroblast growth factor receptor 4 #status predicted <SIG>

F:56-110/Domain: immunoglobulin homology <IM1>

F:132-137/Domain: acidic #status predicted <AD1>

F:177-238/Domain: immunoglobulin homology <IM2>

F:276-347/Domain: immunoglobulin homology <IM3>

F:382-402/Domain: transmembrane #status Predicted <TMM>

F:487-504/Region: protein kinase ATP-binding motif

Query Match	20.8%; Score 455.5; DB 2; Length 822;	Db	559 CTQDGGLYMLVEYASKNLREFL-RARRP--PSPDYTFDMTKVPREQLSFDLVSCSYQV 615
Best Local Similarity	29.2%; Pred. No. 6.3e-16;		
Matches	118; Conservative 82; Mismatches 169; Indels 35; Gaps 11;		
Qy	21 EKQEVTIVPT--LLVTIPLLGYTLWLFIREQTQQRSGPQGIAVPPPRDLSSWEAG 78	Qy	236 LLALBEFLQEQHLFHSDVAARNILMOSDLTAKLGIGLAYEVTRGAISSTOT--IPLKWL 293
Db	383 ETRYDIIITTSGLALLMAAVIVLCRMQLPPTKTHLEATVKLSRFLMROFLESS 442	Db	616 ARGMAYLESRCRICHDLAARNVLVTGENYMKIADEGLARGVHDIDYYKKTSNGRLPKVM 675
Qy	79 HGGNVALPLKETSVENFLGATTPAL-----AKLQVPREQLESEVIL-EQICSGSGC 126	Qy	294 APERILLRPASTRADWMSFGILLYEMVTLGAPPYEVPPTSILEHLQRKRMKRPSSCTH 353
Db	443 SSGKSSTS--VRVPLRSSCTPMLPGVLFEDPLDSKWRPREBL--VIGKPLBEGCRFG 498	Db	676 APEALFDRVYTHQSDWSFGILLWTFLGSFPGIPBELLFKLREGHRMDKDNSCTH 735
Qy	127 PI弗RA--NNNTGDPSPKPSVYLKALKEPAGLHEVQDFLRIOFQHQLGKHNLYQLEG 183	Qy	354 TMYSIMKSCMRWREADRSPSPRELRLRLEAIKTADEAV-LQVP 396
Db	499 QVRAEAYGINKDQDKAITVAKIVKDKGTDDKESDLISEMELKLMGKHNLTNLGV 558	Db	736 ELYMMRECHHAAPSQRPTKQLVETLDRLATVAEYLDLSMP 779
Qy	184 CTEKLPLMMVEDVAGGDLLGFGLWTCRDRDNTMDGLYDUTE-----KVYTHIGKOV 235	RESULT 6	
Db	559 CTQDGGLYMLVEYASKNLREFL-RARRP--PSPDYTFDMTKVPREQLSFDLVSCSYQV 615	TVHIDF	fibroblast growth factor receptor flg-2 precursor - human
Qy	236 LLALBEFLQEQHLFHSDVAARNILMOSDLTAKLGIGLAYEVTRGAISSTOT--IPLKWL 293	N; Contains:	Protein-tyrosine kinase (EC 2.7.1.112) flg-2
Db	616 ARGMAYLESRCRICHDLAARNVLVTGENYMKIADEGLARGVHDIDYYKKTSNGRLPKVM 675	C; Species:	Homo sapiens (man)
Qy	294 APERILLRPASTRADWMSFGILLYEMVTLGAPPYEVPPTSILEHLQRKRMKRPSSCTH 353	C; Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
Db	676 APEALFDRVYTHQSDWSFGILLWTFLGSFPGIPBELLFKLREGHRMDKDNSCTH 735	R; Aviivi, A.; Zimmer, Y.; Yaron, A.; Yarden, Y.; Givol, D.	
Qy	354 TMYSIMKSCMRWREADRSPSPRELRLRLEAIKTADEAV-LQVP 396	A; Title:	Flg-2, a new member of the family of fibroblast growth factor receptors.
Db	736 ELYMMRECHHAAPSQRPTKQLVETLDRLATVAEYLDLSMP 779	A; Reference number:	A60350; PMID:9129390; PMID:1648703
Qy	20.8%; Score 455.5; DB 2; Length 822;	A; Accession:	A60350
Db	20.8%; Score 455.5; DB 2; Length 822;	A; Cross-references:	EMBL:X58255; NID:931382; PID:CAA41209.1; PID:931383
Qy	20.8%; Score 455.5; DB 2; Length 822;	A; Experimental source:	keratinocytes
Db	20.8%; Score 455.5; DB 2; Length 822;	C; Comment:	This may be a receptor for keratinocyte growth factor.
Qy	20.8%; Score 455.5; DB 2; Length 822;	C; Genetics:	
Db	20.8%; Score 455.5; DB 2; Length 822;	A; Gene:	GDB:FGFR2; JWS: CFDL1; KGF: FLG2
Qy	20.8%; Score 455.5; DB 2; Length 822;	A; Cross-references:	GDB:127273; OMIM:176943
Db	20.8%; Score 455.5; DB 2; Length 822;	A; Map position:	10q25.3-10q26
Qy	20.8%; Score 455.5; DB 2; Length 822;	C; Superfamily:	basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
Db	20.8%; Score 455.5; DB 2; Length 822;	C; Keywords:	basic fibroblast growth factor receptor; glycoprotein; growth factor receptor; R; Shi, D.L.; Peige, J.J.; Rion, J.F.; DeSimone, D.W.; Boucalt, J.C.
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 1-21/Domain: signal sequence #status predicted <SIG>	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 22-369/Domain: fibroblast growth factor receptor flg-2 #status predicted <MAT>	
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 22-369/Domain: extracellular #status predicted <EXT>	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 121-137/Region: acidic	
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 262-335/Domain: immunoglobulin homology <IMM>	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 370-390/Domain: transmembrane #status predicted <TM>	
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 391-800/Domain: intracellular #status predicted <INT>	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 412-480/Region: protein kinase ATP-binding motif <KIN>	
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 59-107, 170-222, 269-333/Disulfide bonds: #status predicted	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 96-219, 288, 380, 322/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 504, 519, 611/Active site: Lys, Glu, Asp #status predicted	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 616, 629/Binding site: magnesium (Asn, Asp) #status predicted	
Qy	20.8%; Score 455.5; DB 2; Length 822;	F; 642/Binding site: phosphate (Tyr) (covalent) (by autop phosphorylation) #status predicted	
Db	20.8%; Score 455.5; DB 2; Length 822;	Query Match 20.7%; Score 453.5; DB 1; Length 800;	
Qy	20.8%; Score 455.5; DB 2; Length 822;	Best Local Similarity 30.5%; Pred. No. 7.8e-16; Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;	
Db	20.8%; Score 455.5; DB 2; Length 822;	F; 370-390/Domain: immunoglobulin homology <IMM>	
Qy	21 EKQEVTIVPT--LLVTIPLLGYTLWLFIREQTQQRSGPQGIAVPPPRDLSSWEAG 78	Qy	34 VTFILLIGGYLWLFIREQTQQRSGPQGIAVPPPRDLSSWEAG 78
Db	383 ETRYDIIITTSGLALLMAAVIVLCRMQLPPTKTHLEATVKLSRFLMROFLESS 442	Db	375 VVFIFILVVAVILCRRLSPPKGLGSPVTVKYKSRPLKQYSLNESSMMSNTPL-V 432
Qy	79 HGGNVALPLKETSVENFLGATTPAL-----AKLQVPREQLESEVIL-EQICSGSGC 126	Qy	91 SVENFLGATTPALA--KLQVP-----REQSEVLEQICSGSCGPFRANMTGD 137
Db	443 SSGKSSTS--VRVPLRSSCTPMLPGVLFEDPLDSKWRPREBL--VIGKPLBEGCRFG 498	Db	433 RIARLSSGCPVLLANSELAPPKWLRSRTRLGLGEFGQVMAEAGIDKDR 492
Qy	127 PI弗RA--NNNTGDPSPKPSVYLKALKEPAGLHEVQDFLRIOFQHQLGKHNLYQLEG 183	Qy	138 PSKPVSILKALKERPAQLHEVQDFLGRGQPHOYLGKHNLYQLEGCTEKPLYMLVEDV 197
Db	499 QVRAEAYGINKDQDKAITVAKIVKDKGTDEKESDLISEMELKLMGKHNLTNLGV 558	Db	493 ATCPVTVAYTMRMLKDQDADKSLDLSIVSEMAMKNGKHNLTNLGACTGGPLVLYEA 552
Qy	184 CTEKLPLMMVEDVAGGDLLGFGLWTCRDRDNTMDGLYDUTE-----KVYTHIGKOV 235	Qy	198 AQGDLGFLWTCRDRDNTMDGLYDUTE-----DTEKQVYHIGKQVLLALEFLQEKEL 247
Db	184 CTEKLPLMMVEDVAGGDLLGFGLWTCRDRDNTMDGLYDUTE-----KVYTHIGKOV 235	Db	553 AKGNIRREFL-RARRP---PGMDYSFDACLPPEQLTCKDLSVCAVYARGMEXLASQKC 607

Qy	248	EHGDAARNLIMQSDLTAKLCGIGLAYERVYTRGAISSTQT--IPLKMLAPERLLRPAASI	305	Iberian ribbed newt (fragment)
Db	608	IRHDLAARNVLVTDNVMKIAFGLDVAHNLDYKKTNGRLPVKMAPEALFDVYTH	667	C;Species: Pleurodeles waltlii (Iberian ribbed newt)
Qy	306	RADWWSFGILLYEMVTGAPPKPEVPPTSILEHLQRRKIMKRPSCTTHMTYSIMKSCWRW	365	C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
Db	668	QSDWWSFGILLYEMVTGSPSPGIPVYELFKLKGHRMDKPAASCTHDLIMIMRECWH	727	C;Accession: S38579 R;Shi, D.L.; Promentoux, V.; Launay, C.; Umbhauer, M.; Boucaut, J.C. submitted to the EMBL Data Library, November 1993 A;Description: Expression of FGFR-3 in amphibian embryos.
Qy	366	READRSPREPLRLRLE-AAKPADEAVLQVP	396	A;Reference number: S38579
Db	728	VPSQRTPFKQLVEDLDRLLTVTSDYYDLSSVP	760	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-797 <SHT> A;Cross-references: EMBL:X75603 C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protease inhibitor 7
Qy	204	VENFLGTTPALAKLQVP-----REOLSEVLEQICSSCCGP1FRANNNTGDPSPK	447	Score 447; DB 2; Length 797;
Db	429	LSSDGPMILANVSELELPADPKWELSRSLTLGKPLGEGCPQVWNADAVGIEKDRENKA	488	Best Local Similarity 28.8%; Pred. No. 1.6-15; Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;
Qy	33	LVTIFLILLGVILWLFIREQTOQQRSQGPQGATAPVPPRDLISWEAGHGGNVALPL-KETS	91	Query Match
Db	369	VAVVILVVIITYKMKMPSKETMTAVKVKSPFLKRVQNSMNTPLPYTRITR	428	Best Local Similarity 28.8%; Pred. No. 1.6-15; Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;
Qy	92	VENFLGTTPALAKLQVP-----REOLSEVLEQICSSCCGP1FRANNNTGDPSPK	141	C;Keywords: ATP; growth factor receptor <IMM>
Db	442	KSVIKALKKEPAGLHEVQDFLGRIQFFQYLGRKHNLVQLEGCTTEKLPLMYLEDVQGD	201	F:456-741/Domain: immunoglobulin homology <KIN> F:464-472/Region: protein kinase ATP-binding motif
Qy	142	KSVIKALKKEPAGLHEVQDFLGRIQFFQYLGRKHNLVQLEGCTTEKLPLMYLEDVQGD	201	A;Status: preliminary A;Molecule type: nucleic acid A;Residues: 1-800 <CAT>
Db	489	TSVAVKMLKDDATDKDLSDVSEMMEMKMGKHNIINLLGACTQDQPLVLYEVASKGN	548	A;Cross-references: GR:556291; NID:9298329; PID:AAB25535.1; PID:9298330 A;Experimental source: brain A;Note: sequence extracted from NCBI backbone (NCBIN:126536, NCBIPI:126537) C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protease inhibitor 7
Qy	202	LIGFLWTCRDYNTMDGLY-----DLTEKQVHIGKQVLALEFQEKHLPHGD	251	A;Title: Isolation of the complementary DNA encoding a mouse heparin-binding growth fact
Db	549	LREYL-RARRP---PGNDYSDTCKLPEEQLTFDVKVQARVMEYLASQKCTHRD	603	A;Reference number: A48991 A;Status: preliminary A;Molecule type: protein kinase homology A;Domain: protein kinase homology <KIN> F:472-480/Region: protein kinase ATP-binding motif
Qy	252	VAARNLIMQSDLTAKLCGIGLAYERVYTRGAISSTQT--IPLKMLAPERLLRPASTRADV	309	Query Match
Db	604	LAARNVLYTVDNNVMKIAFDGLARDVHNIDYKKTNGRLPVKMAPEALFDVYTHQSVD	663	Best Local Similarity 30.5%; Pred. No. 7.8e-16; Matches 120; Conservative 71; Mismatches 165; Indels 37; Gaps 9;
Qy	34	VTFILILGVILWLFIREQTOQQRSQGPQGATAPVPPRDLISWEAGHGGNVALPL-KETS	90	RESULT 9
Db	375	VTFILILGVILWLFIREQTOQQRSQGPQGATAPVPPRDLISWEAGHGGNVALPL-KETS	432	Q35963 protein-tyrosine kinase (EC 2.7.1.112) cek2 precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Jul-1999 C;Accession: A35963 R;Pasquale, E.B. Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990 A;Title: A distinctive family of embryonic protein-tyrosine kinase receptors. A;Reference number: A35963; PMID:9032672; PMID:2165604 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-806 <PAS> A;Cross-references: GB:M35195; NID:9211442; PID:9211443 C;Genetics:
Qy	91	SVENFLGTTPALA---RLQVP-----REQLSBEVLEQICSGCIPFRANNNTGD	137	Db
Db	433	RIARLSSGEGPVIANVSELELPADPKWELSRSLTLEKPLGEGCFGQVYMAAIGIDKDR	492	724 RPTFKQIVEDLDRVLTWTSDFYDLSVP
Qy	138	PSPKPSVTKALKKEPAGLHEVQDFLGRIQFFQYLGRKHNLVQLEGCTTEKLPLMYLEDV	197	728 VPSQRTPFKQLVEDLDRLLTVTSDYYDLSSVP
Db	493	TAKPVTAVKMLKDDATDKDLSDVSEMMEMKMGKHNIINLLGACTQDQPLVLYEVAYA	552	RESULT 8
Qy	198	AGQDLIGFLWTCRDYNTMDGLY-----DLTEKQVHIGKQVLALEFQEKHL	247	Qy
Db	553	AGKNLREFL-RARRP---PGNDYSDTCKLPEEQLTFDVKVQARVMEYLASQKCTHRD	607	248 FHGDAARNLIMQSDLTAKLCGIGLAYERVYTRGAISSTQT--IPLKMLAPERLLRPAASI
Qy	248	FHGDAARNLIMQSDLTAKLCGIGLAYERVYTRGAISSTQT--IPLKMLAPERLLRPAASI	305	C;Species: Gallus gallus (chicken) C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Jul-1999 C;Accession: A35963 R;Pasquale, E.B. Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990 A;Title: A distinctive family of embryonic protein-tyrosine kinase receptors. A;Reference number: A35963; PMID:9032672; PMID:2165604 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-806 <PAS> A;Cross-references: GB:M35195; NID:9211442; PID:9211443 C;Genetics:
Qy	306	RADWWSFGILLYEMVTGAPPKPEVPPTSILEHLQRRKIMKRPSCTTHMTYSIMKSCWRW	365	Db
Db	668	QSDWWSFGILLYEMVTGSPSPGIPVYELFKLKGHRMDKPAASCTHDLIMIMRECWH	727	C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protease inhibitor 7
Qy	366	READRSPREPLRLRLE-AAKPADEAVLQVP	396	F:1-23/Domain: signal sequence #status predicted <SIG>
Db	728	VPSQRTPFKQLVEDLDRLLTVTSDYYDLSSVP	760	

F;24-806/Product: protein-tyrosine kinase cek2 #status predicted <EXT>
 F;24-368/Domain: extracellular #status predicted acidic
 F;1-138/Region: acidic C
 C;Superfamily: basic fibroblast growth factor receptor
 C;Keywords: APP; growth factor receptor
 F;262-335/Domain: immunoglobulin homology <IMM>
 F;369-809/Domain: intramembrane #status predicted <INT>
 F;390-806/Domain: intracellular #status predicted <INT>
 F;44-749/Domain: protein kinase homology <KIN>
 F;47-80/Region: protein kinase ATP-binding motif
 F;61-107,170-222,269-332/Disulfide bonds: #status predicted
 F;96,219-256,288,309,329,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;519,611/Active site: Lys, Glu, Asp #status predicted
 F;616,629/Binding site: magnesium (Asn, Asp) #status predicted
 F;612/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match Score 446.5; DB 2; Length 806;
 Best Local Similarity 30.1%; Pred. No. 1.7e-15;
 Matches 118; Conservative 79; Mismatches 164; Indels 31; Gaps 9;

Qy 31 TLLVTFILLGIVLWLFIREORTQQRSFGQTAAPVPPR-DLSWEAGGGNVALPL-K 88
 Db 374 TGLVLFILVPLVITCRMNPKNMKTQVKSKFPLRKQQVSELENNSMNTPLVR 433

Qy 89 ETSVENFLGATTPALAKLQP-----REQLSEVLEQICSSCCGP1FRANNNTGD 138
 Db 434 ITRLSSSDGPMLANVSELEUPDPKWLARSRLTIGKPLGEGCFCQVVMABAIGIDKDP 493

Qy 139 SKPKSVTKALKKEPAGLHEVQDFLGRIQFHQLGKHNLYVQLEGCTEKPLMVLEDY 198
 Db 494 NKAITVAVKMLKDDATDKDSDLVSEEMMMKMGKHNNIINLGLACTQDOPLYVIVEAS 553

Qy 199 QGDLLGFELWTCRDWTMDGILY-----DLTEKQVYHIGKQVLLALEFLOEKHLF 248
 Db 554 RGNIREYL_RARRP---PNDYSDPTCKLQPEEQTFKDVSAYQVARMEYIASQKCI 608

Qy 249 HGDVAARNLTMQSDLTAKLQGLGAYEVYTRGAISSTQ--IPIKWLAPERLLRPASI 306
 Db 609 HRDLAARNVLTEDNMKTAADFLGLARDVNIDYKKTTCRPLPKWMAPELFVRYHQ 668

Qy 307 ADWPSFGILLYEMTGLAPPYPEVPPTSTBLQERKIMRSPSSCTHTNYSIMKSCWRMR 366
 Db 669 SDWSFGLVLINEIFLGGSYPGIVVEELKLLKEGRHMDKPANCTHLYMIRECWHA 728

RESULT 11

TVHUF3 fibroblast growth factor receptor 3 precursor - human
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A38576; A5273; E38469; I51880
 C;Cross-references: GB:M58051; PID:g182568; PID:AAA52450_1; PID:g182569
 R;Keegan, K.; Johnson, D.E.; Williams, L.T.; Hayman, M.J.
 Proc. Natl. Acad. Sci. U.S.A., 88, 1095-1099, 1991
 A;Title: Isolation of an additional member of the fibroblast growth factor receptor family
 A;Reference number: A38576; PMID:9114211; PMID:147508
 A;Accession: A55273; MUID:9214710; PMID:164411
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-806 <KEE>
 A;Molecule type: mRNA
 A;Residues: 76-394, 'V', 396-806 <THO>
 A;Cross-references: GB:M64347; PID:g182564; PID:AAA58470_1; PID:g182565
 A;Note: sequence extracted from NCBI backbone (NCBIP:80226)
 R;Partanen, J.; Maekiae, T.P.; Alitalo, R.; Lehvastaiho, H.; Alitalo, K.
 Proc. Natl. Acad. Sci. U.S.A., 87, 8913-8917, 1990
 A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
 A;Reference number: A38268; MUID:91062389; PMID:2247464
 A;Accession: E38269
 A;Molecule type: mRNA
 A;Residues: 619-675 <PAR>
 A;Cross-references: GB:M37782

RESULT 10

I55363 fibroblast growth factor receptor 3 - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: I55363; sequence_revision 02-jul-1996 #text_change 16-Jul-1999
 R;Ornitz, D.M.; Leder, P.
 J. Biol. Chem. 267, 16305-16311, 1992
 A;Title: Ligand specificity and heparin dependence of fibroblast growth factor receptors
 A;Reference number: I55363; MUID:92355591; PMID:1379504
 A;Accession: I55363
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-801 <RES>
 A;Cross-references: GB:M81342; PID:g199144; PID:AAA19935_1; PID:g199145
 R;Chelliah, A.T.; McEwan, D.G.; Werner, S.; Xu, J.; Ornitz, D.M.
 J. Biol. Chem. 269, 11620-11627, 1994
 A;Title: Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in immunoglobulin
 A;Reference number: A53627; MUID:94209351; PMID:7512569
 A;Accession: B53627
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 242-364 <CHI>
 A;Cross-references: GB:L26492
 C;Genetics:
 A;Gene: mFR3

R; Bellus, G.A.; Hefferton, T.W.; Ortiz de Luna, R.I.; Hecht, J.T.; Horton, W.A.; Machado, Am; J. Hum. Genet. 56, 368-373, 1995
A; Title: Achondroplasia due to recurrent G380R mutations of FGFR3.
A; Reference number: 151880; MUID:95150025; PMID:7847369
A; Accession: I51880
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 361-379 'R' 381-415 <RES>
A; Cross-references: GB:S76733; PID:914201; PID:914202
A; Note: this sequence represents a mutant form associated with achondroplasia
A; Genetics: GDB:FGFR3
A; Gene: GDB:FGFR3
A; Cross-references: GDB:127526; OMIM:100800; OMIM:134934
C; Function:
A; Description: receptor for both acidic and basic fibroblast growth factors
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase C; Key words: ARP; autophosphorylation; duplication; glycoprotein; growth factor receptor; P1-22/Domain: signal sequence #status predicted <SIG>
F; 23-806/Domain: fibroblast growth factor receptor 3 #status predicted <WAT>
F; 376-375/Domain: extracellular #status predicted <EXT>
F; 133-139/Region: acidic
F; 268-341/Domain: immunoglobulin homology <IMM>
F; 376-396/Domain: transmembrane #status predicted <TMM>
F; 397-806/Domain: intracellular #status predicted <INT>
F; 478-486/Domain: protein kinase ATP-binding motif
F; 61-109,176-228,275-339/Disulfide bonds: #status predicted
F; 98,226,291,315,328/Binding site: carboxyhydrate (Asn) (covalent) #status predicted
F; 508,525,617/Active site: Lys, Glu, Asp #status Predicted
F; 622,635/Binding site: magnesium (Asn, Asp) #status predicted
F; 648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
Q; Match Score: 20.3%; Best Local Similarity: 30.5%; Pred. No. 2.3e-15; Matches 117; Conservative 74; Mismatches 15; Indels 32; Gaps 8;
Q; 34 VTFPLILGVILMFLIREPORTQQRSGP---QGIAPIVPPRDLSSWEAGHGGNVALDLEKE 89
*D*b 381 VGFGLFLIIVAATLCHRSPPKKGGSPTVHKISREPLKQVSLESNAHSNTPLVRI 440
*Q*y 90 TSVENFLIGATTTPALAKCQYP-----REQLSEYIEQICSGSGSCSPPIFRANMNTGDP 139
*D*b 441 ARLSSGEGPTLANSELLEPDADPKWELSLPDRKTDLSLIVSEMNMKMGKHNKIINLGACKGPIVLYVYAK 500
*Q*y 140 KPKSVTLLKALKEPAGIHLVHQDFLGRIQFHQLGKHNVLQLEGCCTEKLPLMVDVAQ 199
*D*b 501 KPVTVAVMPLKDADTDXLSDLIVSEMNMKMGKHNKIINLGACKGPIVLYVYAK 560
*Q*y 200 GDLIGFLWTCCRDMVMTMDGLY-----DLTEKVYHIGKQVLLALEFQEKHFH 249
*D*b 561 GNREFL-RARRP---PGLDSFDTCRKPPEQLTFFKDLVSCAYQVARGMEYLASQKCIH 615
*Q*y 250 GDVAARNILMQLSDFLTAKCGIGLAYEVYTRGAISSQT---IPLKWLAPERLILLPASIRA 307
*D*b 616 RDIAARNVNLVTEDNVMKIADEFLGLARDYNDYYKKTNTGRLPVKWMAPEALFDRVYTHQS 675
*Q*y 308 DWWSFGFLVYAVTFLGKAYPTVPPVPTPPTMVKMRPSCTTMYSIMKSCWRRE 367
*D*b 676 DWWSFGFLVWETFTLGGSSPPGPIVPEELFLKLLKEHRMDKPANCTHDLYMIMRECWAAP 735
*Q*y 368 ADPRSPRFRLRLTEAAIK-TADDE 390
*D*b 736 SORPTFKCOLVEDLRVLTVTSTDE 759

RESULT 12
150128 fibroblast growth factor receptor 4 precursor - quail
C; Species: Coturnix coturnix (quail)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C; Accession: I50128
R; Ron, D.; Reich, R.; Checid, M.; Lengel, C.; Cohen, O.E.; Chan, A.M.; Neufeld, G.; Mikl, J. Biol. Chem. 268, 5388-5394, 1993
A; Title: Fibroblast growth factor receptor 4 is a high affinity receptor for both acidic
R; Marceille, C.; Eichmann, A.; Halevy, O.; Breant, C.; Le Douarin, N.M.

RESULT 13
TVHUF4 fibroblast growth factor receptor 4 precursor - human
N; Contains: protein-tyrosine kinase (EC 2.7.1.112)
C; Species: Homo sapiens (man)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R; Partanen, J.; Maekelae, T.P.; Eerola, E.; Korhonen, J.; Hirvonen, H.; Claesson-Welsh, EMBO J. 10, 1347-1354, 1991
A; Reference number: S15345; MUID:91224085; PMID:1709094
A; Accession: S15345
A; Molecule type: mRNA
A; Residues: 1-802 <PAR>
A; Cross-references: EMBL:X57205; PID:CAA40490_1; PID:931371; PID:CAA40490_1; PID:931372
A; Note: binds acidic but not basic fibroblast growth factor with high affinity

A;Reference number: A46615; MUID:93194827; PMID:7680645	Db	595 -QVARGMQYLESRKCIHRDLAARNVLTEDNVMKIADEGLGRLARGYHIDYYKKTSNGRLPV 653
A;Status: nucleic acid sequence not shown; not compared with conceptual translation	Qy	291 KWLAPEPLLPRASTRADWSFGILLWVTVLGAAPPYPERPPPTSLEHLFLRRKIMRKPSS 350
A;Molecule type: mRNA	Db	654 KWWAPAEALPDRVYTHQSDWWSFGILLWELFTLGSPYPGPVEELSLREGHNMDRPH 713
A;Residues: 1-296, 'D', 298-802 <RON>	Qy	351 CTHTMYSIMKSCHWRADRPSPRELRLEAAIKTADDE 390
A;Experimental source: mammary epithelial cell line B5/589	Db	714 CPPENYGLMRECHAPSOPTRFQLVLEADRVILAVSEE 753
A;Note: sequence extracted from NCBI backbone (NCBI:127650)		
A;Note: binds acidic and basic fibroblast growth factors with high affinity		
R;Holtrich, U.; Braeuninger, A.; Strehardt, K.; Ruebmann, Waigmann, H.		
Proc. Natl. Acad. Sci. U.S.A., 88, 1041-1045, 1991		
A;Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member		
A;Reference number: S19225; MUID:92073297; PMID:1720539		
A;Accession: A41598		RESULT 14
A;Status: nucleic acid sequence not shown; not compared with conceptual translation		S51635
A;Molecule type: mRNA		growth factor receptor 2b, keratinocyte growth factor receptor - rat
A;Residues: 399-534, 'M', 536-799, 'SG', 800-802 <HOL>		C;Species: Rattus norvegicus (Norway rat)
A;Experimental source: lung		C;Date: 15-Jul-1995 #sequence revision 21-Jul-1995 #Text_change 16-Jul-1999
R;Partanen, J.; Mäkelä, T.P.; Alitalo, R.; Lehteslaaho, H.; Alitalo, K.		C;Accession: S511635; S511636; S48048; S48047
Proc. Natl. Acad. Sci. U.S.A., 87, 8913-8917, 1990		R;Savagner, P.
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.		submitted to the EMBL Data Library, July 1994
A;Reference number: A38268; MUID:91067389; PMID:2247464		A;Reference number: S51634
A;Accession: D38269		A;Accession: S511635
A;Molecule type: mRNA		A;Status: preliminary
A;Residues: 614-670 <PA2>		A;Molecule type: mRNA
A;Cross-references: GB:M37781		A;Cross-references: EMBL:Z351138; PID:9551271; PIDN:CRAB84510_1; PID:9551272
A;Experimental source: k-562 leukemia cell line		A;Accession: S51636
C;Genetics:		A;Status: preliminary
A;Gene: GDB:RCFR4		A;Molecule type: mRNA
A;Cross-references: GDB:127929; OMIM:134935		A;Cross-references: EMBL:Z351139
A;Molecule position: 5q33.2-5qter		A;Accession: 37-172, 'T', 174-314, 'TV', 315-340, 'T', 342-705 <SA3>
C;Function:		A;Cross-references: EMBL:Z351139; NTD:9551273; PIDN:CRAB84511_1; PID:9551274
A;Description: receptor mediating effects of fibroblast growth factor		R;Savagner, P.; Valles, A.M.; Jouanneau, J.; Yamada, K.M.; Thiery, J.P.
A;Note: expressed in normal lung; expressed in some carcinomas		Mol. Biol. Cell, 5, 851-862, 1994
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote		A;Title: Alternative splicing in fibroblast growth factor receptor 2 is associated with A;Reference number: S48046; PMID:95102150; PMID:7803853
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor		A;Status: preliminary: nucleic acid sequence not shown
F:1-24/Domain: signal sequence #status predicted <SIG>		A;Molecule type: mRNA
F:25-802/Product: fibroblast growth factor receptor 4 #status predicted <MAT>		A;Cross-references: EMBL:Z351139
F:4-13-48/Region: protein kinase ATP-binding motif		A;Accession: S48047
F:10-103/Domain: immunoglobulin homology <IM1>		A;Status: preliminary: nucleic acid sequence not shown
F:165-226/Domain: immunoglobulin homology <IM2>		A;Molecule type: mRNA
F:264-355/Domain: immunoglobulin homology <IM3>		A;Accession: 1-135, 'R', 137-340, 'T', 342-390, 'K', 392-705 <SA4>
F:370-390/Domain: transmembrane #status predicted <TM>		A;Cross-references: EMBL:Z351138
F:495-750/Domain: intracellular #status predicted <INT>		C;Superfamily: basic fibroblast growth factor receptor
F:495-750/Domain: protein kinase homology <KIN>		C;Keywords: ATP; growth factor receptor
F:495-750/Region: protein kinase ATP-binding motif		F:63-648/Domain: immunoglobulin homology <IMM>
F:112-224/271-333/Disulfide bonds: #status predicted		A;Cross-references: EMBL:Z351138
F:503,520,612/Active site: Lys, Glu, Asp #status predicted		F:643/Binding site: magnesium (Asn, Asp) #status predicted
F:617-630/Binding site: phosphate (Tyr) (covalent) (by autop phosphorylation) #status predicted		F:643/3/Binding site: phosphate (Tyr) (covalent) (by autop phosphorylation) #status predicted
Query Match		Query Match
Best Local Similarity 19.8%; Score 434; DB 1; Length 802; Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;		Best Local Similarity 19.8%; Score 413; DB 2; Length 705; Matches 116; Conservative 85; Mismatches 166; Indels 54; Gaps 10;
Db	Qy	19 IQEKEQEVYLIVPIL---VTFILILGVILMPLFIREQT----QQQRQGPQGAP 66
Db	Db	250 VPPPRDLLSWEAGGGNTNPLKETSTVNLGTTPALA-----KLOVPRDOLSE 307
Db	Qy	67 VPPPRDLLSWEAGGGNTNPLKETSTVNLGTTPALA-----KLOVPRDOLSE 115
Db	Db	308 IPRLRQVAESSSSMMNTNPLVRITLSSTGDPMLAGVSEYLPDPKWEPRDQLT- 366
Db	Qy	116 VLEQICSSCGPLFRANRNTGDPSPK---SVTIKALKEPAGIHEQDFLGRIQHQYLIG 172
Db	Db	367 LAKPLGEGFGQVMAEAGIDKDRPQEOSTAVKMDDATEKDLSPLVSEMEMMKG 426
Db	Qy	173 KHONIVLQLEGCCTEKLYPMVLEDVQAGDILGLRLWTFRDMTMGGLYD-----LT 224
Db	Db	427 KHONIVLQLEGCCTEKLYPMVLEDVQAGDILGLRLWTFRDMTMGGLYD-----LT 224
Db	Qy	539 VCTQEGPLVTVIVECAKGNIREFL-RARRPPGPDLSPDRSSEGFLSPFLNSCAY--- 594
Db	Qy	225 EKOVYHHSQVLLAELFQEKHLFHGQDVAARNILMOSDLTAKLCLGGLAYEVYTRGASSSTOT--IPL 290
Db	Qy	233 KQVLLALEFQEKHLFHGQDVAARNILMOSDLTAKLCLGGLAYEVYTRGASSSTOT--IPL 290
Db	484 FKLVLVSTCYQLARGMEYLASQKCIRHDLAARNVLVTEENNVMKIADEGLARDINNDYKK 543	

Job time : 21 secs

RESULT 15

Qy 277 YTRGAISSTOTIPLXKLAPEPLLRLPASIRADWWSFGILLYEMVTTGAPPEPVPPSTIL 336
 Db 548 TING----RLPKVKMNAPEALFDYRTHQSDVWSGVLWEIFLGSPPGIVPEELF 597

Qy 337 EHLQRKIKMRPSSCTHTMYSIMKSOWRREADRSPSPRELRLRAAIKTADEAVLQVP 396
 Db 598 KLLKEGHMDKPTNCINELMMRMDCWHAVPSQRPIFKOLVEDLRLITLTNEEYLDLT 657

Qy 397 E 397
 Db 658 Q 658

Query Match 19.8%; Score 433; DB 2; Length 707;
 Best Local Similarity 27.9%; Pred. No. 7 3e-15; Mismatches 165; Indels 56; Gaps 10;
 Matches 118; Conservative

Qy 19 IOEKQEYIVYPTLL----VTEFLILIGYLWLFREBQTQQRSGPQGIA----- 65
 Db 250 VREK-BTTASDYLEIAIYCIGVFLIACMVTVTIFCRMKTTKEDFSSQPAVHLTKR 307

Qy 66 -PVPPPDRDLSWBAGHGNVALPLKETSVENFLGATPALA----- KLOVPREQL 113
 Db 308 IPLRRQTVTSAESSSSMNNTPLVRITRLSSTADPMLAGYSEYELEPDPKWEFFRDKL 367

Qy 114 SBEVLEQICSGSCGPPIKANMNTGDPSKPK--SVVILKALKEAGLHEVQDFLGRIGQHQY 170
 Db 368 T-LGKPDLGEGCFCGVVMMAEVGIDKDCKPKEAVTVAKMLKDATEKDLSLVSEMEMMMK 426

Qy 171 LGKHKNLVQLEGGCTKEPLKMYLVEDVAQGDULGFINTCREDVMTMDGLYD----- 222
 Db 427 IGRHRKNIILGACTQDPLVVIVETVAYASGNIREYARRPGMEYS---YDINRVPEEQ 483

Qy 223 LTKQVYHIGKVLLALEFLQEKHLPHGDAARNLIMQSDLTAKLCLGLA-----Y 274
 Db 484 MTFKDLYSTCYQLARGMEYLAQKCTHRDLARNVLTENNVMKIAFGIARDINNDYY 543

Qy 275 EYVTRGRASSSTQTIPKLAPERLLPASTRADWWSGILLYEMVTLGAPPPEPVPPS 334
 Db 544 KKTNTG----RLPVKWMMAPEALFDRYTHQSDVWSGVLWEIFLGSPGPVVEE 597

Qy 335 TLBLHQFRKIMGRPSSCTHTMYSIMKSOWRREADRSPSPRELRLRAAIKTADEAVLQ 394
 Db 598 LPKLLKEGHMDKPTNCINELMMRMDCWHAVPSQRPIFKOLVEDLRLITLTNEEYLD 657

Qy 395 VPE 397
 Db 658 IHQ 660

Result No.	Score	Query Match	Length	DB ID	Description
1	2192	100.0	422	14	US-10-040-884-3
2	2188	99.8	458	15	US-10-240-145-67
3	1079	49.2	209	9	US-09-862-027-6
4	542	24.7	104	9	US-10-836-382-24
5	452	20.6	93	9	US-09-864-761-45860
6	444	20.3	806	12	US-10-403-161-58
7	444	20.3	806	15	US-10-394-322A-28
8	444	20.3	808	12	US-10-403-161-60
9	443	20.2	694	16	US-10-302-812-46
10	434	19.8	802	9	US-09-758-336-3
11	434	19.8	802	14	US-10-011-148-33
12	434	19.8	802	14	US-10-354-158-44
13	434	19.8	802	15	US-10-114-275-245
14	434	19.8	802	15	US-10-394-322A-29
15	434	19.8	802	16	US-10-302-812-48

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2192	100.0	422	14	US-10-040-884-3
2	2188	99.8	458	15	US-10-240-145-67
3	1079	49.2	209	9	US-09-862-027-6
4	542	24.7	104	9	US-10-836-382-24
5	452	20.6	93	9	US-09-864-761-45860
6	444	20.3	806	12	US-10-403-161-58
7	444	20.3	806	15	US-10-394-322A-28
8	444	20.3	808	12	US-10-403-161-60
9	443	20.2	694	16	US-10-302-812-46
10	434	19.8	802	9	US-09-758-336-3
11	434	19.8	802	14	US-10-011-148-33
12	434	19.8	802	14	US-10-354-158-44
13	434	19.8	802	15	US-10-114-275-245
14	434	19.8	802	15	US-10-394-322A-29
15	434	19.8	802	16	US-10-302-812-48

Software: FastSEQ for Windows Version 3.0

SEQ ID NO: 3

TYPE: PRT

ORGANISM: Homo sapiens

NUMBER OF SEQ ID NOS: 6

LENGTH: 422

QUERY MATCH

100.0%

Score: 2192;

DB: 14;

Length: 422;

Best Local Similarity

100.0%

Pred. No. 1

8-e-190;

Mismatches

0;

Gaps

0;

Indels

0;

;

;

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;

RESULT 1

US-10-040-884-3

; Sequence 3, Application US/10040884

; Publication No. US2003007822A1

; GENERAL INFORMATION:

; APPLICANT: ZENECA Limited

; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE

; FILE REFERENCE: 70332/US/Substantive

; CURRENT APPLICATION NUMBER: US-10/040,884

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: US/09/310,438

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 60/088,958

; PRIOR FILING DATE: 1998-06-11

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 3

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ALIGNMENTS

QY 181 EGCCTEKPLPLYLEDVAGDLIGFLWTCRDRDMGGLYDILTEKQYHTIGQVLLALE 240
 Db 181 EGCCTEKPLPLYLEDVAGDLIGFLWTCRDRDMGGLYDILTEKQYHTIGQVLLALE 240
 QY 241 FLOEKHLPHGDYAARNILMOSDTLTAKLCLGLAYEVTGALSSTOTPLKWLAPERLL 300
 Db 241 FLOEKHLPHGDYAARNILMOSDTLTAKLCLGLAYEVTGALSSTOTPLKWLAPERLL 300
 QY 301 RPASIRADWMSFGLLYEMTTLGAPPEVPTTSILEHQLQRKIMKRPSSTHTMYSIMK 360
 Db 301 RPASIRADWMSFGLLYEMTTLGAPPEVPTTSILEHQLQRKIMKRPSSTHTMYSIMK 360
 QY 361 SCWRREADRSPRELRURLEAKTADAEVLQVPELVPPLYAAVAGIRVELFVNYS 420
 Db 361 SCWRREADRSPRELRURLEAKTADAEVLQVPELVPPLYAAVAGIRVELFVNYS 420
 QY 421 ML 422
 Db 421 ML 422
 QY 457 ML 458

RESULT 3
 US-09-862-027-6
 ; Sequence 6, Application US/098662027
 ; Patent No. US20020142428A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hodge, Martin R.
 ; TITLE OF INVENTION: NO. US20020142428A1 Kinases and uses Thereof
 ; FILE REFERENCE: 35000/234862
 ; CURRENT APPLICATION NUMBER: US/09/862,027
 ; CURRENT FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: US 09/345,473
 ; PRIOR FILING DATE: 1999-06-30
 ; NUMBER OF SEQ ID NOS: 82
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 6
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-862-027-6

Query Match 49.2%; Score 1079; DB 9; Length 209;
 Best Local Similarity 100.0%; Pred. No. 1e-89; Mismatches 0; Indels 0; Gaps 0;

QY 214 MTMDGLLXDLTETQQVYHIGKQVLLALELQEKGHLFGDVAARNILMOSDTLTAKLGLGLIA 273
 Db 1 MTMDGLLXDLTETQQVYHIGKQVLLALELQEKGHLFGDVAARNILMOSDTLTAKLGLGLIA 60
 QY 274 YEVYTRGAISSTOTPLKWLAPERLLPASTRADWNSFGILLYEMTILGAPPYPEVPT 333
 Db 61 YEVYTRGAISSTOTPLKWLAPERLLPASTRADWNSFGILLYEMTILGAPPYPEVPT 120
 QY 334 SILEHLQRKIMKRPSSTHTMYSIMSCWRREADRSPRELRURLEAKTADAEVL 393
 Db 121 SILEHLQRKIMKRPSSTHTMYSIMSCWRREADRSPRELRURLEAKTADAEVL 180

RESULT 4
 US-09-86-392-24
 ; Sequence 24, Application US/09836392
 ; Patent No. US200201345BA1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polypeptides, a
 ; FILE REFERENCE: PTO2001
 ; CURRENT APPLICATION NUMBER: US/09/836,392
 ; CURRENT FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/28066
 ; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 60/159,542
 ; PRIOR FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: 60/165,914
 ; PRIOR FILING DATE: 1999-11-17

QY 1 MGMRMLLESLSDKLCLVIOEQKEVITIPTPLTYLTVLFLILLGVLLWFIREQTOQQSG 60
 Db 37 MGTRMILLESLSDKLCLVIOEQKEVITIPTPLTYLTVLFLILLGVLLWFIREQTOQQSG 96
 QY 61 PGATAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQPREQSEVLEQI 120
 Db 97 PGATAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQPREQSEVLEQI 156
 QY 121 CGSGCGPITPRANMNTGDPSPKPSVTKLALKEPAGIHEVDFLGRKQYHIGKHNLYQL 180
 Db 157 CGSGCGPITPRANMNTGDPSPKPSVTKLALKEPAGIHEVDFLGRKQYHIGKHNLYQL 216
 QY 181 EGCCTEKPLPLYLEDVAGDLIGFLWTCRDRDMGGLYDILTEKQYHTIGQVLLALE 240
 Db 217 EGCCTEKPLPLYMLEDVAQCDLIGFLWTCRDRDMGGLYDILTEKQYHTIGQVLLALE 276
 QY 241 FLOERHLPHGDYAARNILMOSDTLTAKLCLGLAYEVTGALSSTOTPLKWLAPERLL 300

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; PRIOR APPLICATION NUMBER: 60/189,027
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 24
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-03-836-392-24

; NUMBER OF SEQ ID NOS: 49117 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 45660
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021049_1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EST HUMAN HIT: H08599_1, EVALUATE 3.0ne-05
; OTHER INFORMATION: SWISSPROT HIT: P77580, EVALUATE 8.40e-01
; US-03-864-161-45860

Query Match Score 542; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5e-41;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 MVTLGAPPYEVPPPTSILEHILQRKIMKRPSSCTHTMYSIMKSCMRWREADRSPRELRU 378
Db 1 MVTLGAPPYEVPPPTSILEHILQRKIMKRPSSCTHTMYSIMKSCMRWREADRSPRELRU 60

Query Match Score 452; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.3e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 379 RLEAAAKTDAV1QPELVPELYAAVGAVIRVESTFNYSM1 422
Db 61 RLEAAAKTDAV1QPELVPELYAAVGAVIRVESTFNYSM1 104

RESULT 5
US-09-864-761-45860
; Sequence 45860, Application US/09864761
; Patent No. US20030048763A1

Query Match Score 452; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.3e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 IAPVPFRDLSWEAGHGGNVALPKETSVENFLGATTPALAKLQVPREQLESEVLEQICSG 123
Db 1 IAPVPFRDLSWEAGHGGNVALPKETSVENFLGATTPALAKLQVPREQLESEVLEQICSG 60

Query Match Score 452; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.3e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 SCGP1FRANNNTGDPSPKSVILKALK 150
Db 61 SCGP1FRANNNTGDPSPKSVILKALK 87

RESULT 6
US-10-403-161-58
; Sequence 58, Application US/10403161
; Publication No. US20040043930A1
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; CURRENT APPLICATION NUMBER: US/10/403,161
; FILE REFERENCE: 21402-573C
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/3722019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/479679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/374379
; SOFTWARE: CurateSeqList version 0.1
; SEQ ID NO: 58
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-403-161-58

Query Match Score 444; DB 12; Length 806;
Best Local Similarity 30.5%; Pred. No. 3.e-31;
Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-29
; PRIOR FILING DATE: 2001-01-29
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: CurateSeqList version 0.1
; SEQ ID NO: 58
; LENGTH: 806
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-403-161-58

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Query 34 VTFILILGVILNLFIREQRTQQQRSGP---QGIAVPVPPRDLSSWEAGHGGNNVALPL-KE 89
 Database 381 VCPFLFILVAATLICRSPPKKGLOSSPTVKISRPLKQVSLSNASMSNTPLVRI 440

Query 90 TSVENFLGATTTPALAKLQYP-----REQLSEVTEEQICSGSCGPIFRAMNTGDP 139
 Database 441 ARLSSEGEGPTLANVSSELLPADPKWELLSRARLTGKPLGEFCGQVMAEAGIDKORAA 500

Query 140 KPKSVLILKALKEPAGLHEVQDFLRLIQFQYGLKHNIVQLLEGCTERLPLPLYLVEDAQ 199
 Database 501 KPVTAVKMLKDADTKDLSLVSEMEMKMKIGKHKNINLLGACTQGGPLVVEYAKA 560

Query 140 KPKSVLILKALKEPAGLHEVQDFLRLIQFQYGLKHNIVQLLEGCTERLPLPLYLVEDAQ 199
 Database 501 KPVTAVKMLKDADTKDLSLVSEMEMKMKIGKHKNINLLGACTQGGPLVVEYAKA 560

Query 200 GDLIGFLWTCRDVNTMKGGLY-----DLTEKQYHIGKVQVLLALEFQKHLFH 249
 Database 616 RDLAARNVLTEDVMKIADEGLARDVNLDYKRTTNGRQLPKWMAEALFDRVYTHQS 735

Query 250 GDYAARNLIMOSDITAKLCLGLAYEVTRGAISSTOT--IPLKWLAPERLIRPASTRA 307
 Database 616 RDLAARNVLTEDVMKIADEGLARDVNLDYKRTTNGRQLPKWMAEALFDRVYTHQS 675

Query 308 DWWSFGILLYVOMTLGAPPYYPEPPTSLLEHQLRKIMKRPSSCTHMYSIMKSCWRE 367
 Database 676 DWWSFGVLWIEITLGSSGPYGPVPEELFKLREGHMDKPANCTHDLYMTRCWHAA 735

Query 368 ADPSPSPRLRLREAK-TADDE 390
 Database 736 SQRTFFQLOVEDIDRVYTHQS 759

RESULT 7
 US-10-394-322A-28
 ; Sequence 28, Application US/10394322A
 ; Publication No. US2003022391A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SONESIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
 ; CURRENT APPLICATION NUMBER: US/10/394-322A
 ; CURRENT FILING DATE: 2003-03-20
 ; PRIORITY FILING DATE: 2002-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 28
 ; LENGTH: 806
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-394-322A-28

Query Match 20.3%; Score 444; DB 15; Length 806;
 Best Local Similarity 30.5%; Pred. No. 3_4e-31;
 Matches 117; Conservative 74; Mismatches 161; Indels 32; Gaps 8;

Query 34 VTFILILGVILNLFIREQRTQQQRSGP---QGIAVPVPPRDLSSWEAGHGGNNVALPL-KE 89
 Database 381 VGFPLFILVAATLICRSPPKKGLOSSPTVKISRPLKQVSLSNASMSNTPLVRI 440

Query 90 TSVENFLGATTTPALAKLQYP-----REQLSEVTEEQICSGSCGPIFRAMNTGDP 139
 Database 443 ARLSSEGEGPTLANVSSELLPADPKWELSRARLTGKPLGEFCGQVMAEAGIDKORAA 502

Query 140 KPKSVLILKALKEPAGLHEVQDFLRLIQFQYGLKHNIVQLLEGCTERLPLPLYLVEDAQ 199
 Database 503 KPVTAVKMLKDADTKDLSLVSEMEMKMKIGKHKNINLLGACTQGGPLVVEYAKA 562

Query 200 GDLIGFLWTCRDVNTMKGGLY-----DLTEKQYHIGKVQVLLALEFQKHLFH 249
 Database 563 GNLEFL-RARRP---IGLDISFTCKPPEEQTFFDVLSCVARGMEYLASQKCIH 617

Query 250 GDYAARNLIMOSDITAKLCLGLAYEVTRGAISSTOT--IPLKWLAPERLIRPASTRA 307
 Database 618 RDLAARNVLTEDVMKIADEGLARDVNLDYKRTTNGRQLPKWMAEALFDRVYTHQS 677

RESULT 9
 US-10-302-812-46
 ; Sequence 46, Application US/10302812
 ; Publication No. US20040087016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating et al.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND TISSUE REGENERATION
 ; FILE REFERENCE: HYDR-P02-004
 ; CURRENT APPLICATION NUMBER: US/10/302, 812
 ; CURRENT FILING DATE: 2002-11-21
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 46
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-302-812-46

Query Match 19.8%; Score 434; DB 9; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 21 EKQEYIVV---PTLAVTFLILGVLWLFIREORTQQORSGP---QGIAVPVRPRDL 73
 ; SEQ ID NO: 3
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 19.8%; Score 434; DB 9; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 364 EARYTDILLYASGSIALVILLAGL 74
 ; SEQ ID NO: 4
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 19.8%; Score 434; DB 9; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 419 SLEESSSGKSSSLVGRVLISSGPALLAGLVSLLDPLWEPDRDLVLGKPGEGCF 478
 ; SEQ ID NO: 5
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 19.8%; Score 434; DB 9; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 479 GQVRAEAFMGDPARDQASTVATMVKONASDKDADLVSEEMVKLGTRHONLTNLIG 538
 ; SEQ ID NO: 6
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 19.8%; Score 434; DB 9; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 539 VCTQEGPLVYVIVECAKGUNLREFL-RARPPPGPDSBGPSSSGPISPVULSYCAY--- 594
 ; SEQ ID NO: 7
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 44 ILWLFIREQTQQORSGPQGIAPVPPRDLWEAHHGGNVALPL-KETSVENFLGATTAA 102
 ; SEQ ID NO: 8
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 285 IQWL-KHVVEVGSKVGPDD-TPYTVLKVSLSNASMSNTPLVRIARUSGGPTLAN 341
 ; SEQ ID NO: 9
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 103 LAKLQVP-----REOLSEVYLEQICGSSCPPIFRAMNTGDPSKPKSVILKALKEP 152
 ; SEQ ID NO: 10
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 342 VSELFLPADTKWELSRARLTGKPGEGCGQVVMMAEIGIDKRAKEPVTVATMQLDD 401
 ; SEQ ID NO: 11
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 453 AGLHEVQDFGIGRIQFHQYLGLGKHNLYQVLSGCCTEKLPLIMVLDVAQGDLGLGFILWTCRD 212
 ; SEQ ID NO: 12
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 402 ATDKDLSLIVSEMNMKMKHGKHNLYQVLSGCCTEKLPLIMVLDVAQGDLGLGFILWTCRD 460
 ; SEQ ID NO: 13
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 213 VMTMDGLY-----DLTEKOVYHIGKQVLLIALEFIIQKHLFGHQDVAAINTLMD 262
 ; SEQ ID NO: 14
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 461 ---PGLDYSFDTCKPPEECOLTDVLVSQAYQVARGMEVIALQSCKTHRLAARNVLVED 516
 ; SEQ ID NO: 15
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 263 LTAKLQGLGLAYEVYTRGAISSTO-----IPLKWLAPERLURPASTRADYWSFGFLILYEMV 320
 ; SEQ ID NO: 16
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 517 NVMKIADFGIARDVHNLDYKKITNGRLPKWMPAEFLPDRVYTHQSDWWSFGWLWLF 576
 ; SEQ ID NO: 17
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 321 TLGAPPYPVPPSTSLEHLQRKRMKRPSSCTHTMYSIMKSCWNRREADPSPRELRUJ 380
 ; SEQ ID NO: 18
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 577 TLGSPYRGPVPEELFKLKGHRMDKPANCNTDLYMIRNECWFAAPSQSRPTQLVEDL 636
 ; SEQ ID NO: 19
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 381 EAALK-TADDE 390
 ; SEQ ID NO: 20
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

Query Match 20.2%; Score 443; DB 16; Length 694;
 Best Local Similarity 30.7%; Pred. No. 3.4e-31;
 Matches 114; Conservative 71; Mismatches 154; Indels 32; Gaps 9;

Qy 637 DRVLTVTSDE 647
 ; SEQ ID NO: 21
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-758-386-3

RESULT 10
 US-09-758-386-3
 ; Sequence 3, Application US/09758386
 ; Patent No. US20010016335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc. et al.
 ; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-5
 ; FILE REFERENCE: PF486PCT
 ; CURRENT APPLICATION NUMBER: US/09-758, 386
 ; CURRENT FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: 09/293, 182
 ; PRIOR FILING DATE: 1999-04-16

RESULT 11
 US-10-011-548-33
 ; Sequence 33, Application US/10011548
 ; Publication No. US20030055218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Timans, Jacqueline C.
 ; DEBETS, Johannes Eduard Maria Antonius
 ; Sana, Theodore R.
 ; Baran, J. Fernando Kastelein, Robert A.
 ; TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 ; NUMBER OF SEQUENCES: 36
 ; CURRENT APPLICATION DATA:
 ; ADDRESS: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10-011, 548
 ; FILING DATE: 22-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/173, 151

FILING DATE: <Unknown>
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0767X

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)852-9196
 TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
 LENGTH: 802 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. US20030055218A1 Relevant

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 33:
 US-10-011-548-33

Query Match 19.8%; Score 434; DB 14; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

21 EKOEYIVV---PTLLVTFPLLGVLWLFIREQRTQQQRSGP---QGIAVPVPPRDL 73
 364 EARYTDIILYASGLSLAAVLLAGL---YRGQALHGRHRPPTVQLSRFLARQF 418

74 SWEAGHGGNVNVLPL-KETSVENFLGATTPALAKLQVPREQLSF----VLEQICSGSC 125
 419 SLESGSSSSKSSSLVRGVTRLSSGPALLAGLVSLLDLPMEFPRDRVLGKPLGECCF 478

126 GPIFRANNNTGDPSKP---KSYVTKALKKEPAQHLYEVDFGLRIQFHQYGHKNLYLEG 182
 479 GQVRAAEFGMDPARDQASTAVMRKDNDASDDKDLADLVSEMEVMKLIGHEKNLNLG 538

Db 183 CCTEKPLIYMLVEDVAQGDLGLFWTCRDV--MTMDG-----LLYDLTEKQYHIG 232
 539 VCTQEGLPYIVIVECAARCNLRFL-RARRPGPDLSGPSSGPRLSPVLSVSCAY--- 594

Db 233 KOVLLALEFLQEKHLFHQDVAARNLIMQSDLTAKLKGIGLAVEYVYRGAISSTQT--IPL 290
 595 -QVARGMQLYLESRKCIHDLAARNLVLYEDNMVKIADEGLARGVHHTDYYKKTSNGRLPV 653

Db 291 KWLAPEILLRPLPASTIRDVTHQSWSFGILLWIFITUGGSPPGIPYEEFLSILREGRHMDEPH 713
 654 KWNAPEAFLDRTVTHQSWSFGILLWIFITUGGSPPGIPYEEFLSILREGRHMDEPH 713

Db 351 CTHTMYSIMKSCWRWREADRSPSPRELRLRLEAIKTADE 390
 714 CPDELYGLMRECWHAAPSORPTFKQLVADKVLAYSEE 753

RESULT 12
 US-10-354-318-44
 Sequence 44, Application US/10354358
 Publication No. US20030157082A1

GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc
 APPLICANT: MacBeth, Kyle J.
 APPLICANT: Tsai, Pong-Ying
 APPLICANT: Leson, Andrea

Db 714 CPPELYGLMRECWAAPSQRPFKQLVEALDKVLLAVSEE 753

RESULT 13
 US-10-116-275-245
 ; Sequence 245, Application US/10116275
 Publication No. US20030211476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Daragh, Byrne, Daragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and
 CURRENT APPLICATION NUMBER: US/10/116,275
 FILE REFERENCE: E106/20087
 CURRENT FILING DATE: 2002-10-04
 NUMBER OF SEQ ID NOS: 349
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 245
 LENGTH: 802
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-116-275-245

Query Match 19.8%; Score 434; DB 15; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 21 EKQEYIVIV--PTLVLTFILLGVILWLFIREORTQQRSGP---QGIAPVPPRDL 73
 364 EARYTDILYASGLALAVLLAGL---YRGQALHGRHPRPATTQKLSPREPLAQF 418

Db 74 SWEAGHGGNVALPL-KETSVENFLGATTPALAKLQVPREQLESE----VL-EQICSGSC 125
 419 SLESSSGKSSSLVRGVRLSSGPALLAGIVSLDLPLWEPFRDLVLGPKLGECCF 478

Qy 74 SWEAGHGGNVALPL-KETSVENFLGATTPALAKLQVPREQLESE----VL-EQICSGSC 125
 419 SLESSSGKSSSLVRGVRLSSGPALLAGIVSLDLPLWEPFRDLVLGPKLGECCF 478

Db 126 GPIFRANNNTGDPSKP--KSVILKALKEPAGILEHVQDFLGRCIQHQYLGRHNVLQLEG 182
 479 GQVRAEAFGMDPARDQASTAVAVMLKDQNSDKDADLYSEMEYMKLGRHNVNLLG 538

Qy 183 CCTEKPLPLYLEDVAQDGLLGFILWTCRRDV--MTMDG-----LLYDLTEKQYTHIG 232
 539 VCTQERPLPYLVIVECAKGNRREFL-RARRPGPDLSPDGRSSECPLSFPVLSVCAV-- 594

Db 233 KQVLLALEFLOEKHLFHGDYAAARNLIMQSDLTAKLGLGIAVEYVTGAISSSTQT-IPL 290
 595 -QVARGMQYLESRKCITHDLAARNVLTENVMKLADEFGIARGVHIDYRKTKTSNGRLPV 653

Qy 291 KWLAPPLRPLPASITPDWSEFGILLYEMTUGAPPEVPPTSILLEHORRKTMKRPSS 350
 654 KWMAPALFDRVYTHQSDVWSFGILWELITGGSPGPVVEELFSLLREGHMRDRPH 713

Db 351 CTHTMYSIMKSCMWRREADPSPRELRLDEAAIKTADDE 390
 714 CPPELYGLMRECWAAPSQRPFKQLVEALDKVLLAVSEE 753

Qy 126 GPIFRANNNTGDPSKP--KSVILKALKEPAGILEHVQDFLGRCIQHQYLGRHNVLQLEG 182
 479 GQVRAEAFGMDPARDQASTAVAVMLKDQNSDKDADLYSEMEYMKLGRHNVNLLG 538

RESULT 15
 US-10-302-812-48
 ; Sequence 48, Application US/10302812
 ; Publication No. US20040087016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating et al.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
 ; TITLE OF INVENTION: TISSUE REGENERATION
 ; FILE REFERENCE: HYDR-P02-004
 ; CURRENT APPLICATION NUMBER: US/10/302,812
 ; CURRENT FILING DATE: 2002-11-21
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 48
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-302-812-48

Query Match 19.8%; Score 434; DB 16; Length 802;
 Best Local Similarity 29.8%; Pred. No. 2.7e-30;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Qy 21 EKQEYIVIV--PTLVLTFILLGVILWLFIREORTQQRSGP---QGIAPVPPRDL 73
 364 EARYTDILYASGLALAVLLAGL---YRGQALHGRHPRPATTQKLSPREPLAQF 418

Db 74 SWEAGHGGNVALPL-KETSVENFLGATTPALAKLQVPREQLESE----VL-EQICSGSC 125
 419 SLESSSGKSSSLVRGVRLSSGPALLAGIVSLDLPLWEPFRDLVLGPKLGECCF 478

Qy 126 GPIFRANNNTGDPSKP--KSVILKALKEPAGILEHVQDFLGRCIQHQYLGRHNVLQLEG 182

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Db    479 GQYVRAFGMPARPDQASTAVKMLRDNSDKDADLVSEMEVNKLIGRHKNIINLGLG 538
Qy    183 CCTEKLPIYVLEDVAQDLIGFLWTRRDV--MTMDG-----LLYDLTEKOVYHIG 232
Db    539 VCTQEGPLIVVTCAGNLRFEL-RARRPPGFDLSPDGRSSEGPIISFPVLVSCAY--- 594
Qy    233 KOYLLALEFLOEKHLIFHGDAARNLIMOSDLTAKLCGGLGAYEVYTRGAISSTOT--IPL 290
Db    595 -QVARGMYLESKCIRHDLAARNVLVEDNMKIADEGLARGVHHIDYRKTSNGRLPV 653
Qy    291 KWLAPELILLRPASTRADWWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRKIMKRSS 350
Db    654 KWNAAPEALFLDRVYTHQSOWWSFGILLWIFLGGSPYGPVVEELFSILREGRHMRDPH 713
Qy    351 CHTHMYSMKSCWRWREADRSPRELRLRLEAIKTADE 390
Db    714 CPPBLYGLMRECWHAAAPPORPTFKOLYEDKULLAYSEE 753

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Search completed: June 14, 2004, 18:51:43
 Job time : 50 secs

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OM protein - protein search, using sw model

Run on: June 14, 2004, 18:43:09 ; Search time 22 Seconds
(without alignments)
990.280 Million cell updates/sec

Title: US-10-040-884-3
Perfect score: 2192
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing First 45 summaries

Database : Issued Patents AA:
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 5: /cgm2_6/ptodata/2/iaa/PCUTS_COMB.pep *
 6: /cgm2_6/ptodata/2/iaa/backfiles/pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1079	49.2	209	4	US-09-345-473B-6
2	444	20.3	801	3	US-09-383-530-6
3	444	20.3	806	3	US-09-383-530-3
4	435	19.8	310	2	US-08-701-131A-8
5	435	19.8	310	4	US-09-664-526-8
6	434.5	19.8	378	1	US-08-070-165F-8
7	434.5	19.8	378	2	US-08-885-418-8
8	434	19.8	802	4	US-09-173-51A-33
9	433	19.8	652	1	US-08-471-570-10
10	427	19.5	821	2	US-08-451-522A-13
11	427	19.5	821	4	US-08-323-530-13
12	424	19.3	729	1	US-07-640-029-3
13	424	19.3	731	1	US-08-921-807B-4
14	424	19.3	731	1	US-08-441-94A-5
15	424	19.3	731	3	US-08-439-932A-3
16	424	19.3	733	1	US-07-60-029-4
17	424	19.3	733	1	US-07-921-807B-6
18	424	19.3	733	1	US-08-441-94A-6
19	424	19.3	733	3	US-08-439-932A-6
20	424	19.3	820	1	US-07-921-807B-4
21	424	19.3	820	1	US-08-441-94A-3
22	424	19.3	820	3	US-08-439-932A-1
23	424	19.3	822	1	US-07-997-933-1
24	424	19.3	822	1	US-07-921-807B-4
25	424	19.3	822	2	US-08-441-94A-4
26	424	19.3	822	3	US-08-439-932A-12
27	424	19.3	822	3	US-08-439-932A-2

RESULT 1
US-09-345-473E-6
; Sequence 6, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-345-473E-6

Query Match 49.2%; Score 1079; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 8.2e-91; Mismatches 0; Indels 0; Gaps 0;

Query Match 214 MTMDGLYDITEKQVYHIGQVLLALEFQEKHIFGHGDYARNITLMSDILTAKLGGLGA 273
Db 1 MTMDGLYDITEKQVYHIGQVLLALEFQEKHIFGHGDYARNITLMSDILTAKLGGLGA 60
Qy 274 YEVVTRGATTSQTQPLKWLAPERLLRPAStRADWWSFGTLLYEMVTLGAPPVEPPT 333
Db 61 YEVVTRGATTSQTQPLKWLAPERLLRPAStRADWWSFGTLLYEMVTLGAPPVEPPT 120
Qy 334 SILEHLQRKRKIMKRPSSCTHTMYSIMKSQRWRADPSPREPLRLRLEAKTADDEAVL 393
Db 121 SILEHLQRKRKIMKRPSSCTHTMYSIMKSQRWRADPSPREPLRLRLEAKTADDEAVL 180
Qy 394 QVPVELVPELYAAVAGIRVESLFNYNSML 422
Db 181 QVPVELVPELYAAVAGIRVESLFNYNSML 209
RESULT 2
US-09-383-630-6
; Sequence 6, Application US/09383630A
; Patent No. 62265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yanon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
 STREET: 2001 Jefferson Davis Highway, Suite 207
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22202

COMPUTER READEABLE FORM: 3.5" microdisk
 COMPUTER: Twinhead* SImmote-890TX
 OPERATING SYSTEM: MS DOS version 6.2,
 SOFTWARE: Word for Windows version 3.11
 to an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/383,630A

FILING DATE: 26-Aug-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA: <Unknown>

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 1402/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

TELEFAX: 972-3-5625554

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 801

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-383-630-6

Query Match 91 SVENFLGNTTPALA---KLQVP-----REQLSEVLEQICSGSGPIRANMNTGD 137

Best Local Similarity 30.5%; Prod. No. 5.0e-32; Length 801;

Matches 120; Conservative 71; Mismatches 165; Indels 38; Gaps 10;

Qy 34 VTFILLGVILWLFIREQRTQQRSGQGIAPV---PPPRDLWSWEAGHGGNVNVALPLKET 90

Db 375 VVFFLFLIVVAATLCLRSPPKGLGSPTVKVSFRFLKQVSLSENNSMSNTPL-V 432

Qy 433 RIALRSSGPVIANSEELPAPKWNLSRTRLGPBLGEGCFCGVYMAAIGIDKDR 492

Db 138 PSKPKSVLKAKEPAAGHEVQDFLGRQFHQLGKKNLVQLEGCTEKPLMYLEDV 197

Qy 493 TAKPVTVAVKMLKDATHKDLSLVSEMEMMMKGKHKNITNLGACTQGGPLVLYEA 552

Db 198 AQDGLLGWTCTRDVMMDGLY-----DLPKQVTHIGKQVTLAELFQEKHL 247

Qy 553 AKGNLREFL-RARRP---PGMDYSFDACRLPEQLTCKDLSVCAQVARGMEYLASQKC 607

Db 248 FRGDVAANTIMOSDLTAKLGLGLAYVYTRGAISSTOT--IPLXWLAPEUILLRPSIRA 305

Db 608 IHRDLAANRNLVTEDNVKIADEGLARIDVHNLDYVKKCTNGRPVKAPEALFDRVYTH 667

Qy 306 RADYWPSGILLYEMVTLGAP-PYPEVPTSILEHLQRKIMRPSSCTHTMYSIMKSCWR 364

Db 668 QSDWWSFVLLWIFTPGSPSPGIPPEELFKLKGCHRMDKPASCTHDYIMRECWH 727

Db 365 WRBADRPSPREBLRL--AAIKTADDAVLQVP 396

Qy 728 AVFSQRPTEKOLVEDLRLTVTSTDEYLDLSVP 761

Db 501 KPVTAIVKMLKODATAKDLDSLVSEMEMMMKGKHNIILIGACTQGGPLVLYEAQ 560

Qy 200 GDIGELMTCRDVMMDGLY-----DITEKQVYHIGKQVVLAAEFLQEKHLFH 249

Db 561 GNREFL-RARRP---PGLDYSDTCKPPERQTLFDLVSAYQVARGMEYLASQKC 615

Qy 250 GDVARNILMQSDLTAKLGLGLAYVYTRGAISSTOT--IPLXWLAPEUILLRPSIRA 307

Db 616 RDIAARNVLTENVKIADEGLARIDVHNLDYKCTNGRPVKAPEALFDRVYTH 675

Qy 308 DWSGFLGYAVNLGAP-PYPEVPTSILEHLQRKIMRPSSCTHTMYSIMKSCWR 367

Db 676 DWSGVLLWEIFTLGESPYPGIPPEELFKLKGHRMDKPANCTHDLYMINRECWHAA 735

RESULT 3

US-09-383-630-3

Sequence 3, Application US/09/383,630A

; Patent No. 6265632

; GENERAL INFORMATION:
 ; APPLICANT: Avner Yavon et al.; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
 ; FACTOR RECEPTOR ASSOCIATED
 ; CHONDRODYSPLASIA

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
 ; STREET: 2001 Jefferson Davis Highway, Suite 207
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: United States of America

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

; COMPUTER: Twinhead* SImmote-890TX

; OPERATING SYSTEM: MS DOS version 6.2,

; Windows version 3.11

; SOFTWARE: Word for Windows version 2.0 converted

; to an ASCII file

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 megabye, 3.5" microdisk

; COMPUTER: Twinhead* SImmote-890TX

; OPERATING SYSTEM: MS DOS version 6.2,

; Windows version 3.11

; SOFTWARE: Word for Windows version 2.0 converted

; to an ASCII file

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/383,630A

; FILING DATE: 26-Aug-1999

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Friedman, Mark M.

; REGISTRATION NUMBER: 33,883

; REFERENCE/DOCKET NUMBER: 1402/2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 972-3-5625553

; TELEFAX: 972-3-5625554

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 806

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

; US-09-383-630-3

Query Match 34 VTFILLGVILWLFIREQRTQQRSGP---QGIAVPPPPRDLWSWEAGHGGNVNVALPL-KE 89

Best Local Similarity 20.3%; Score 444; DB 3; Length 806;

Matches 117; Conservative 30.5%; Pred. No. 5.7e-32; Mismatches 161; Indels 32; Gaps 8;

Qy 381 VGFFLFLIVVAATLCLRSPPKGLGSPTVHKISREPLKRQVSLSNASMSNTPLVRYI 440

Db 90 TSVBNFGATTPLAKLQVP-----REQSEVLEQICSGSCOPFRANNTGDP 139

Qy 441 ARLSGEGPTLANSEELPADPKWELSRARLTGRLGEFGQVTMMAEGIDKORA 500

Db 140 KPKSVTKLKEPAAGHEVQDFLGRQFHQLGKKNLVQLEGCTEKPLMYLEDV 199

Db 501 KPVTAIVKMLKODATAKDLDSLVSEMEMMMKGKHNIILGACTQGGPLVLYEAQ 560

Qy 250 GDVARNILMQSDLTAKLGLGLAYVYTRGAISSTOT-IPLXWLAPEUILLRPSIRA 307

Db 616 RDIAARNVLTENVKIADEGLARIDVHNLDYKCTNGRPVKAPEALFDRVYTH 675

Qy 308 DWSGFLGYAVNLGAP-PYPEVPTSILEHLQRKIMRPSSCTHTMYSIMKSCWR 367

Db 676 DWSGVLLWEIFTLGESPYPGIPPEELFKLKGHRMDKPANCTHDLYMINRECWHAA 735

Qy 368 ADPSPRELRLRLEAAIK-TADDE 390
Db 736 SORPFQOLVEDIDRVTUTSTDE 759

RESULT 4
US-08-701-191A-8
; Sequence 8, Application US/08701191A
; Patent No. 5912428

GENERAL INFORMATION:
; APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,191A
; FILING DATE: August 21, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 3,2,327
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 227/088
; TELEPHONE: (213) 489-1600
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-701-191A-8

Qy 327 YPEVPPTSILEHQLQRKIMKRPSSCTHTMYSIMKSCKMRREADPSPRELRLRLEAAIK- 385
Db 246 YPGIPVEELFKLKEGRMRDPAANCYDLYMIMRECWHAAAPSQRPTFKQLVEDLDRVLTV 305

RESULT 5
US-09-664-526-8
; Sequence 8, Application US/09664526
; Patent No. 662921
; GENERAL INFORMATION:
; APPLICANT: MOHAMMADI, MOOSA
; ADDRESS: SCHLESSINGER, JOSEPH
; STREET: HUBBARD, STEVEN R.
; CITY: TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
; STATE: LOS ANGELES
; COUNTRY: CALIFORNIA
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/664,526
; FILING DATE: 2000-09-18
; PRIORITY NUMBER: 09/188,809
; PRIOR FILING DATE: 1998-11-09
; PRIORITY NUMBER: 08/701,191
; PRIOR FILING DATE: 1996-08-21
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-664-526-8

Query Match 19.8%; Score 435; DB 4; Length 310;
Best Local Similarity 33.4%; Pred. No. 1e-31; Indels 20; Gaps 6;
Matches 102; Conservative 62; Mismatches 121;

Qy 101 PALAKUQPREQLS-EVLEQICSSCGP-FRANNNTGDSKPKSVILKALKEPAGLHEV 158
Db 11 PADPKWELSLARLTGKPLGEGCFCQVVMMAIGIDKDKRAAKPVTVAVRMLKDDATDKDL 70

Qy 159 QDFLGRRIQFOYLGKHKNLYQLEGCCTEKPLPMLVEDAQGDLLGFMTCRDVMMDG 218
Db 71 SDLVSEMEMKMKIGKHNINLGLCTQGPPLYVYAKGNUREFL-RARRP---PG 125

Qy 219 LLY-----DITEKQYTHIGKQVLALEFLOEHLFHGDVAARNNTLMSODITAKLC 268
Db 126 LDYSEDTCKPPEEQTLTKOIVSCAYQVARGMEYLASQKCIHRDIAARNVLTEDNMVKIA 185

Qy 269 GLGLAYEVYTRGAISSTQT-IPLKWLAPRLRASRADWNSGILLYEMVTLGAPP 326
Db 186 DFGLARDVNLDYRKTTNGRLPKVWAPALFRVYTHEQSDWSFGVLLWEFTLGGSPP 245

Query Match 19.8%; Score 435; DB 2; Length 310;
Best Local Similarity 33.4%; Pred. No. 1e-31; Indels 20; Gaps 6;
Matches 102; Conservative 62; Mismatches 121;

Qy 327 YPEVPPTSILEHQLQRKIMKRPSSCTHTMYSIMKSCKMRREADPSPRELRLRLEAAIK- 385
Db 246 YPGIPVEELFKLKEGRMRDPAANCYDLYMIMRECWHAAAPSQRPTFKQLVEDLDRVLTV 305

RESULT 6
US-08-070-165F-8
; Sequence 8, Application US/08070165F
; Patent No. 5750365
; GENERAL INFORMATION:
; APPLICANT: Chiu, Ing-Ming
; ADDRESS: Boulin, Matthew L.
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aRGF)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Ing-Ming Chiu
 STREET: S2052 Davis Medical Research Center, 480 West
 CITY: Columbus
 STATE: Ohio
 COUNTRY: USA
 ZIP: 43210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/070,165F
 FILING DATE:

CLASSIFICATION: 435
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (614)-293-5631
 TELEX: (614)-293-8093

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-070-165F-8

Query Match Score 434.5; DB 1; Length 378;

Best Local Similarity 32.7%; Pred. No. 1.5e-31;
 Matches 102; Conservative 66; Mismatches 123; Indels 21; Gaps 7;

DB 27 PADERWEIJRSRSLTGLPKGEGRGQVVMDAVIGIERKPKNATTAVAKMQLKDATDKDL 86

QY 101 PALAKLQVPREQLS--EVLEQICSGCGPIFRANMTGDPSPKSVILKALKEPAAGHEV 158

DB 87 SDLVSEMMMKMGKHNNTINLGGACTQDGPLYVLYEYASKNLREYL-RARRP---PG 141

QY 219 LLY-----DLTERQVYHIGKOYLLAFLQEKHLFHEDVAARNLIMOSDLTAKLC 268

DB 202 DFGARDYHNDIYKCTNGRLVKWNAPEALDRVTYHQSDWSFGYLLWEFTLGSP 261

QY 269 GLGLAYEYTRGAISSQT--IPLKWLAPERLLRPASTRADYWSFGILLYEMVTLGAPP 326

DB 142 MDYSFDTCKLPEEQLTFKDVLSCAYQVARGMEYLASQKTCIRHDLAARNVLTDNNMKIA 201

QY 219 LLY-----DLTERQVYHIGKOYLLAFLQEKHLFHEDVAARNLIMOSDLTAKLC 268

DB 202 DFGARDYHNDIYKCTNGRLVKWNAPEALDRVTYHQSDWSFGYLLWEFTLGSP 261

QY 327 YPEVPPSTILEHLQRKRIMKRPSSCTHTMYSIMKSCKNRWEADRSPRELRLEAAIK- 385

DB 262 YPGIPVEBLFKLKEGHMRDKPANCTHLYMIMRECHWAPSOPTFKQLVEDDLRVITV 321

RESULT 7
 US-08-070-165F-8

Sequence 8, Application US/09173151A

Patent No. 5925528
 GENERAL INFORMATION:
 APPLICANT: Chiu, Ing-Ming
 APPLICANT: Poulin, Matthew L

NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ing-Ming Chiu
 STREET: 9th Avenue

CITY: Columbus
 STATE: Ohio
 COUNTRY: USA
 ZIP: 43210

RESULT 7
 US-08-0885418-B
 Sequence 8, Application US/08885418
 Patet No. 5925528
 GENERAL INFORMATION:
 APPLICANT: Chiu, Ing-Ming
 APPLICANT: Poulin, Matthew L
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Acidic Fibroblast Growth Factor (aFGF)
 STREET: 9th Avenue
 CITY: Columbus
 STATE: Ohio
 COUNTRY: USA
 ZIP: 43210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/885,418
 FILING DATE:
 CLASSIFICATION: 435
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (614)-293-8093
 TELEFAX: (614)-293-5631
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-885-418-8

Query Match Score 434.5; DB 2; Length 378;
 Best Local Similarity 32.7%; Pred. No. 1.5e-31;
 Matches 102; Conservative 66; Mismatches 123; Indels 21; Gaps 7;
 DB 27 PADPKWELSRSLTGRPLBEGFGQVVMDAVIGIEEKPKNATAVKMLKDATDKDL 86

QY 101 PALAKLQVPREQLS--EVLEQICSGCGPIFRANMTGDPSPKSVILKALKEPAAGHEV 158

DB 87 SDLVSEMMMKMGKHNNTINLGGACTQDGPLYVLYEYASKNLREYL-RARRP---PG 141

QY 219 LLY-----DLTERQVYHIGKOYLLAFLQEKHLFHEDVAARNLIMOSDLTAKLC 268

DB 142 MDYSFDTCKLPEEQLTFKDVLSCAYQVARGMEYLASQKTCIRHDLAARNVLTDNNMKIA 201

QY 269 GLGLAYEYTRGAISSQT--IPLKWLAPERLLRPASTRADYWSFGILLYEMVTLGAPP 326

DB 202 DFGARDYHNDIYKCTNGRLVKWNAPEALDRVTYHQSDWSFGYLLWEFTLGSP 261

QY 327 YPEVPPSTILEHLQRKRIMKRPSSCTHTMYSIMKSCKNRWEADRSPRELRLEAAIK- 385

DB 262 YPGIPVEBLFKLKEGHMRDKPANCTHLYMIMRECHWAPSOPTFKQLVEDDLRVITV 321

RESULT 8
 US-09-173-151A-33

Sequence 33, Application US/09173151A
 Patent No. 6326472
 GENERAL INFORMATION:
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNA Research Institute
 STREET: 901 California Avenue
 STATE: California
 CITY: Palo Alto
 COUNTRY: USA
 ZIP: 94304-1104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/173,151A
 FILING DATE: 14-OCT-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/065,776
 FILING DATE: 17-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,008
 FILING DATE: 12-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/081,883
 FILING DATE: 15-APR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/095,987
 FILING DATE: 10-AUG-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/078,416
 FILING DATE: 18-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/062,066
 FILING DATE: 15-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DR0767X
 TELEPHONE: (650) 498-1200
 TELEFAX: (650) 498-9196
 SEQUENCE CHARACTERISTICS:
 LENGTH: 802 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-173-151A-33

Query Match 19.8%; Score 434; DB 4; Length 802;

Best Local Similarity 29.8%; Pred. No. 4.6e-31;
 Matches 119; Conservative 77; Mismatches 164; Indels 40; Gaps 12;

Db 364 EARYDILYASGLALAVILLAGH---YRGQALHGGERPPATVQLSRFLARQF 418

Qy 74 SWEAGHGNVALPL-KETSYENFLGATTPLAKLQVPRBUSE-----VL-EQICSGSC 125

Db 419 SLESGSSGKSSSLVRGVRLSSGGALLAGIVSDLPLDFLWEFRDLVKGRLGECCP 478

Qy 126 GPFDANMNTGDPSPKP--KSVILKEAFLKEAGLHEVQDFGRIGRQHICKHKNLVOLEG 182

Db 479 QGYVRAEAFGMMPDQASSTVAVMLKDASDKDADLVSEMEYMLGIRHKNLNLIG 538

Qy 183 CCTERKLPLMVLEDYQAGDLIGFLGKFWRDRLV---MTMDG-----LIVDLTKEQVHIG 232

Db 539 VCTQEGPLVYVECAKGNRREFL-RARRPGDPLSPDRGSSEGPLSPVLYSCAY--- 594

Qy 233 KQVLLALEFTQEKHLFHGDVAARNILMQSTDUTAKUGLGIAVEYTRGAISSTOP--IPL 290

Db 595 -QVARGMQLYESRKCFTHRDIAARNVLYTEVNVMKIADEGLARGVHIDYKKTSNGRLPV 653

Qy 291 KWLAPEBLRQPLPASTRADWVSGTLLQRRKIMKRPSS 350

Db 654 KWMAEAFLFVRYTHQDSWVSGTLLWEITFLGSPGPVVEELFLSLREGHMRDPRPH 713

Qy 351 CTHTMYSIMKSCWNRREADPSPRELRLLEAAALKTADDE 390

Db 714 CPPPEYLGLMRECWHAPSOPTFKOLVVEALDKVLLAVSEE 753

US-08-471-570-10 ; Sequence 10, Application US/08471570
; Patent No. 5150371 ;
; GENERAL INFORMATION:
; APPLICANT: IGRASHI, Koichi
; APPLICANT: SENOO, Masaharu
; APPLICANT: WATANABE, Tatsuya
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,570
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,564
; FILING DATE:
; APPLICATION NUMBER: US 07/7433369
; FILING DATE: 16-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: LINEK, Ernest V
; REGISTRATION NUMBER: 29822
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 40897
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6400
; TELEX: 200291 STRE UU
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 652 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-570-10

Query Match 19.8%; Score 433; DB 1; Length 652;
 Best Local Similarity 28.0%; Pred. No. 4.3e-31;
 Matches 115; Conservative 82; Mismatches 162; Indels 52; Gaps 9;

Qy 22 KOYEVTIVPTL-----VTEFLILGCVLWLFREORT-----QQRSGPQGTAPVPP 69
 Db 251 REKEITASPDYLEIAIYCIGVFLACMVYTVLGRMKNTTKKPDFSQFAVHLTKRIPU 310

Qy 70 PRDLSWEAHGNVALPLKETSVENFLGTTPAIA-----KLQYPREQSEYLE 118
 Db 311 RQYSAESSSSMSNTPLVYTRITRLSSTADTPMLAGSVEYELPDPKWEFPDLT-LGK 369

Qy 119 QICSGSGPFRAMNTGDPSPKP--SVLKALKEPAGLHEYQDFLGRQHQYLGKHK 175
 Db 370 PLGBGFQVMAEAVGIDDKPKEAVTAVRMKRDDATEKLDLSVSEMEMMMKMKIGKHK 429

Qy 176 NLVQLEGCGCTEKPLPYMLVEDVAGDGLLGFLWCRDWTMMDGLYD-----LTKQ 227
 Db 430 NTINLGAQCTDGFLVYVEYASKNREYLARRPMEYNS---YDINRVPEEQMTPKD 486

Qy 228 VYHIGQVLLALEPQKHFLFGDVAAVNLMOSDSTARLKGIGLA-----YEYTR 279
 Db 487 LVSTCYQLARGMEYLASQXCIHDLAARNVLTENNVMKIADEGLARDINNIYVKTN 546

Qy 280 GAISSTOTIPKWLAPERILLRPAStIRADWVSGFILYEMVTLGAPPYPEVPPTSILEHL 339

547 G-----ELPKVKRNPAAPELFDRVYTHQDMWIFLGGSPVPGIPVEELFKLL 600
 340 QRKIMKRPSSCTHTMYSIMKSCMRWRADPSPRELRLRLEAKTADDE 390
 ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ; : ;
 601 KEGRMDKEANCNTNELMMRDCWHAVPSQRPTFKOLVEDLDRILTTNE 651
 RESULT 10
 Sequence 13, Application US/08451822A
 GENERAL INFORMATION:
 APPLICANT: Dionne, Craig A
 APPLICANT: Crumley, Greg
 APPLICANT: Jaye, Michael C
 APPLICANT: Schlessinger, Joseph
 TITLE OF INVENTION: Fibroblast Growth Factor Receptors
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Legal Department
 STREET: 500 Arcola Road
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/451,822A
 FILING DATE: 26-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/323,430
 FILING DATE: 14-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/934,372
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/549,587
 FILING DATE: 06-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Savitzky, Martin
 REGISTRATION NUMBER: 29,699
 REFERENCE/DOCKET NUMBER: A0496E
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3816
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 821 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 Sequence 13, Application US/08451822A-13
 RESULT 11
 US-08-323-430-13
 ; Sequence 13, Application US/08323430
 ; Patent No. 6344546
 ; GENERAL INFORMATION:
 ; APPLICANT: Dionne, Craig A
 ; APPLICANT: Crumley, Greg
 ; APPLICANT: Jaye, Michael C
 ; APPLICANT: Schlessinger, Joseph
 ; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
 ; STREET: 500 Arcola Road
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/323,430
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/323,430
 ; FILING DATE: 21-AUG-1992
 ; APPLICATION NUMBER: US 07/549,587
 ; FILING DATE: 06-JUL-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goodman, Rosanne
 ; REGISTRATION NUMBER: 32,534
 ; REFERENCE/DOCKET NUMBER: A0496E
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 454-3817
 ; TELEFAX: (215) 454-3808
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 821 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 Query Match 19.5%; Score 427; DB 2; Length 821;
 Best Local Similarity 27.4%; Pred. No. 2.1e-30;
 Matches 115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;
 22 KQYEVLIVPTL----VTFILGLIVLWLFIREQTQQRSQQGIA-----PV 67
 365 REKEITASPDYLEIAIYCIGFELIACMVTIVLCKRMNTKKPDESSQAVHKLTKRIPL 424
 68 PPRDLSWEAGHGENVALPLKETSVENFLGATTPLA-----KLOVPREQLSEV 116
 425 RRQTVTAESSESSMSNSNTPLVRITRISSTDTPMLATGSEYELDPKWEFRDKLT-L 483
 117 LEQICSGCGCIFRANNMTGDPSKP---SVLKALKEPAGLHEVDFGRIOPHOYLGSK 173
 Query Match 19.5%; Score 427; DB 4; Length 821;
 Best Local Similarity 27.4%; Pred. No. 2.1e-30;
 Matches 115; Conservative 84; Mismatches 167; Indels 54; Gaps 9;
 22 KQYEVLIVPTL----VTFILGLIVLWLFIREQTQQRSQQGIA-----PV 67

Db 365 REKEITASPPDYLEAIYCTGVLLACMVVVILCMMKNTYKPDFFSQPAVHKLTKRIPL 424

Qy 68 PPPRDLNSWFAHHGGNVALPKETSVENFLAGTATTPLA-----KQVPREOJSEV 116

Db 425 RROVTVSAEASSSSMNSNTPLVIRTRLSSATDTPMLAGVSEYELPEDPKWEFPDKLT-L 483

Qy 117 LEQICSGSGPPIFRANMNTGDPSPK-----SIVLKALKEPKGLHEVQDFLGRIOFQYLGH 173

Db 484 GRPLGECCGCGQVMMAEVGIDKDKEPEAVTVAVKMLKDDTEKDLSLIVSEMEMMKMIGK 543

Qy 174 HNLVQLBECCTERPLPMLVLEDVAQGDLLGFATCRDWTMDGLYD-----LTE 225

Db 544 HKNINLIGACTQDGPLTYIVEASKGNIREYLARRPPEMEYS--YDINRVPBEQMTF 600

Qy 226 KQVTHIGKQVLLALEFQEKLHFGDVAARNLIMQSDLTAKLCGLA-----YEYV 277

Db 601 KDLVSCRYQLARGMEYLASQCKTHRLAARNVLYTENNWKIADEGLARDINNDYYKCT 660

Qy 278 TRGAISSTQTIPKWLAPERLILRPASTRADWISFGILLEMVTGAPPVPEVPPTSLIE 337

Db 661 TNG-----RLPVTKWMPAFLFORVYTHQSDVWLMWEEIFLGGSYGPVPEELEK 714

Qy 338 HLRQRKIMKRPSSCTHTMYSIMKSCWRPREDRPLRLRAAIKTADEAVLQVE 397

Db 715 LKEKGHRMDKPANCNTNLYMMMRDCWHAVPSQRPTFKQLVYDLDLTTNEEYLDLQ 774

RESULT 12

US -07-640-029-3

; Sequence 3, Application US/07640029

; Patent No. 5229501

; GENERAL INFORMATION:

; APPLICANT: Kiefer, Michael C.

; APPLICANT: Valenzuela, Pablo D. T.

; APPLICANT: Barr, Phillip J.

; TITLE OF INVENTION: Expression and Use of Human Fibroblast

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/640,029

; FILING DATE: 1993-01-11

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: McClung, Barbara G.

; REGISTRATION NUMBER: 33,113

; REFERENCE/DOCKET NUMBER: 0209.001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-2708

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 731 amino acids

; TYPE: amino acid

; STRANDEDNESS: Single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US -07-640-029-3

Query Match 19.3%; Score 424; DB 1; Length 729;

Best Local Similarity 30.2%; Fred. No. 3.3e-30;

Matches 97; Conservative 67; Mismatches 127; Indels 30; Gaps 5;

Qy 100 TPAL-----KLUQVPRQ-----

Db 361 TMLAGVSEYELPEDPRWELPDRVLGKPLGBCGFGQVLAEAIGLDKDPNRVTKVAV 420

Qy 147 KALKEPAGLHEVQDFLGRIQFHQLYKHLVOLLEGCCCTEKPLXMYMLEVEDAQGHLGFL 206

Db 421 RMLKSDATEKDLSLISEMEMMMKIGKREKNTINLGAQCTDGPVIVTEYASKQNRELY 480

Qy 207 WTCRRDVTMDSLY-----DLTEKQVTHIGKQVLLALEFLOEKHLFHSDVAARN 256

Db 481 QARR----PPGLEXYCYNPSHNFEEQLSSKDLVSCAYQVARGNEYASKKC1HRLDAARN 535

Qy 257 TLMQSDLTAKUGLGLAYEVTRGAISSTQT-IPKWLAPERLILRPASTRADWISFGI 314

Db 536 VLVTEENVMKTADEFGLARDIHIDYKKTNGRLPVKVNMAPEALFDRTYTHQSLWWSFGV 595

Qy 315 LLYEMVTLGAPPYEPVPTSLIEHLQRKIMKRPSSCTHTMYSIMKSCWRREADRPSPR 374

Db 596 LLWEFTFLGGSPYPGPVVEELFKLLEKGHRMDKPANCNTNLYMMRDCHAVPSQRPTFK 655

Qy 375 ELRLRLLEAAIAKTPADDRAVLQV 395

Db 656 QLVEDDRIVALTNSQSYLDL 676

RESULT 13

US -07-921-807B-5

; Sequence 5, Application US/07921807B

; Patent No. 5474914

; GENERAL INFORMATION:

; APPLICANT: SPEBETE, RICHARD

; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION

; STREET: 4560 Horton Street - R440

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608-2916

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/921, 807B

; FILING DATE: 29-SEP-1992

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McClung, Barbara G.

; REGISTRATION NUMBER: 33,113

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-2708

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 731 amino acids

; TYPE: amino acid

; STRANDEDNESS: Single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US -07-921-807B-5

Query Match 19.3%; Score 424; DB 1; Length 731;

Best Local Similarity 30.2%; Fred. No. 3.3e-30;

Matches 97; Conservative 67; Mismatches 127; Indels 30; Gaps 5;

Qy 100 TPAL-----KLUQVPRQ-----

363 TPLLAGVSEYELPEDPRMELPDRDLVLGKPLGECCFGQVVLAAEAGLDKDKPNRVTKAV 422 Db

147 KALKPEGHLVEQDFLGRIFHQYLGRKHNLVQLEGCTEKPLMVLEDVAQGDLGLFL 206 Qy

423 KMLKSDATEKDLSLISEMEMMMKMGKHNLINLLGACTQDGPLVYVTEASKGNUREVL 482 Db

207 WTCRDVMTMDGLY -----DLTEKOVHIGKQVLLIALEFLQEKHLFGDVAARN 256 Qy

483 QARR -----PPGLECYNPSHNPPEQLSKODLVSCAYQVARMEYLASKCICHRDLAARN 537 Db

257 ILMQSDLTAKLGLCLAYEVTRGAISSTQT- -IPLKWLAPERLILRPASTRADWNSFGI 314 Qy

538 VLVETDNVKLADFLGLARDIHHIDYYKTTNGRLPVKWMAPBELLFRYTHQDWSFGV 597 Db

315 LLYEMVTLGAPPYPEYPTTSILEHLQRKIMKRPSCTHTMYSIMKSCWRWREADRSPR 374 Qy

598 LLWEITLGSSPYGPYGVPEELFKLKEGHMDKPSNTLYMMEDCWTAPEQSQPTFK 657 Db

375 ELRLRLEAIAKTADEAVLQV 395 Qy

658 QLVDEDLDRIVALTTSNQRYLDL 678 Db

RESULT 14
US-08-441-944A-5
; Sequence 5, Application US/08441944A
; Patent No. 5767250
; GENERAL INFORMATION:
; APPLICANT: SPAETE, RICHARD
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,944A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,807
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCULLING, BARBARA G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0209.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-944A-5

Query Match Score 424; DB 1; Length 731;
Best Local Similarity 30.2%; Pred. No. 3.3e-30;
Matches 97; Conservative 67; Mismatches 127; Indels 30; Gaps 5;

RESULT 15
US-08-439-992A-3
; Sequence 3, Application US/08439992A
; Patent No. 6255454
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Pablo, Valenzuela D.T.
; APPLICANT: Philip, Barr J.
; TITLE OF INVENTION: Expression and Use of Human Fibroblast
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,992A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 0165.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2704
; TELEX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-439-992A-3

Query Match Score 424; DB 3; Length 731;
Best Local Similarity 30.2%; Pred. No. 3.3e-30;
Matches 97; Conservative 67; Mismatches 127; Indels 30; Gaps 5;

100 TPALAA-----KLOVPREQ--LSELEQICSGSCGPFRANNNTGDPSPKSVIL 146 Qy

363 TPMAGVSEYLPEDPRWELLVKGPKLDPKPNRVTKAV 422 Db

Qy 147 KALKEPAGLHEVQDFELGRIOFHQYLGKHKHKNLVQLEGCCTEKLPLIMVLEPDVAOGDILGFFL 206
 Db 423 KMLKSDATERDSLISSEMMEMMRIGKHKNINLNLLGACTQGPVLVIVETASKGNLREYL 482
 Qy 207 WTCRRDVMTMDGLLY-----DLTEKQYHIGKQVNLALLEFLQEKEHLFHGDVAARN 256
 Db 483 QARR----PPEGLEXYCNPSHNPEBLOSSCDLVSCLAYQVARGMEYLASKCTHRDLAARN 537
 Qy 257 ILMOSDILTAKLGLGLAYEVTRGAISSTQT--IPLKWLAPERLLRPASTADWWSFGI 314
 Db 538 VLVTEDDNVKLADFGGLARDIHHDYYKKTTNGRLPVKWWMAPEALDRIYTHOSDWWSFGV 597
 Qy 315 LLYEMWTLGAPPYPEVPPTSLEHJLORKTMKRPSSCHTMYSTINKSCWRREADRSPR 374
 Db 598 LLWEIFTLGSSPYPGYPVEELFKLKEGHRMDKPSNCTNELYMMNRDCWHAVPSOPTFK 657
 Qy 375 ERLRPLEAAIKTADDEAVLQV 395
 Db 658 QLVEDLDRIVALTSNOEYLDL 678

Search completed: June 14, 2004, 18:46:52
 Job time : 23 secs

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GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: June 14, 2004, 18:37:48 ; Search time 58 Seconds
 (without alignments)
 2055.777 Million cell updates/sec
 Title: US-10-040-884-3
 Perfect score: 2192
 Sequence: 1 MGNTRMILECSLSDKLCVHQ.LYAAVAGIRVESLIFYNSM 422
 Scoring table: BIOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 1586107 seqs, 282547505 residues
 Total number of hits satisfying chosen parameters: 1586107
 Minimum DB seq length: 0

max/min DB seq length: 2000000000

No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score being printed, and is derived by analysis of the totality of the distribution.

Result No.	Query			Length	DB	ID	Description
	Score	Match	%				
1	2192	100.0	422	3	AAY44297		Aay44297 Human rec
2	2192	100.0	495	4	AAB65706		Aab65706 Novel pro
3	2189	99.9	422	3	AAY44299		Aay44299 Human rec
4	2188	99.8	458	4	AAU68537		Aau68537 Human nov
5	2183	99.6	422	4	AAGG6404		Aag6404 Human fib
6	2176	99.3	421	3	AAY44298		Aay44298 Human rec
7	1079	49.2	209	4	AAB6603		Aab6603 Human b14
8	743	33.9	183	4	AAB5707		Aab5707 Novel pro
9	542	24.7	104	4	AAE00672		Aae00672 Human pro
10	452	20.6	93	4	ABBA3239		Aabb3239 Peptide #
11	452	20.6	93	4	AAIB37079		Aam37079 Peptide #
12	452	20.6	93	4	AAM76972		Aam76972 Human bon
13	452	20.6	93	4	AAM64146		Aam64146 Human bra
14	452	20.6	93	4	ABGS8633		Abg8633 Human liv
15	444	20.3	801	4	AAE21977		Aae21977 Mouse fib
16	444	20.3	806	4	AAB21976		Aab21976 Human fib
17	444	20.3	806	6	ABA38646		Abj38646 FGFR3 pro
18	444	20.3	806	6	ADAB8050		Adab8050 Human FGF
19	444	20.3	806	6	AAB36462		Aab36462 Human FGF
20	443	20.2	694	5	ABG66739		Abg66739 Human nov
21	435	19.8	526	5	AAI15269		Aai15269 Clone PTB
22	435	19.8	687	2	AAY06456		Aay06456 2NF198 FG
23	434.5	19.8	378	2	AAW37805		Aaw37805 Fibroblas
24	434.5	19.8	378	2	AAY23632		Aay23632 New fib
25	434	19.8	802	5	AAE16588		Aae16588 Human fib

ALIGNMENTS

RESULT 1
AY44297
ID AY44297 Standard; protein; 422 AA.

AAY44297;
29-FEB-2000 (first entry)
Human receptor tyrosine kinase.

Human: receptor tyrosine kinase; RTK; tyrosine kinase modulator; signal transduction tyrosine kinase; Cdc2 kinase; mitosis; tumour; cancer; adenocarcinoma; brain; Alzheimer; RTK associated disorder; adenocarcinoma; angiogenesis; arthritis; diabetic retinopathy; ischaemic heart disease; atherosclerosis; inflammation.

Homo sapiens.

SUMMARIES

Aay44297 Human rec
Aab65706 Novel pro

/label= extracellular-domain
 /label= "can be used for screening therapeutic compounds"
 26. 422

/label= Cytoplasmic domain
 /label= "intracellular functional domain which can be used for screening therapeutic compounds"
 123. 422

/label= Tyrosine_kinase_domain
 /label= "can be used for screening therapeutic compounds"

AA	PN	W09964589-A1.		
	XX			
	PD	16-DEC-1999.		
	XX			
	PF	08-JUN-1999;	99WO-GB001798.	
	XX			
	PR	11-JUN-1998;	98US-0088958P.	
	XX			
	PA	(ZENE) ZENeca LTD.		
	XX			
	PI	Childay N.	Panchamoorthy G;	
	XX			
	DR	WPI; 2000-097538/08.		
		N-PSDR. AA229332		
		NNNN		

XX New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.
PT cancers for treating adenocarcinoma.
XX Page 49-50; 56pp; English.
PS Claim 11; Page 49-50; 56pp; English.

The present sequence is a human receptor tyrosine kinase (RTK) which activates Cdc2 kinase that mediates mitosis. Tyrosine kinase is selectively expressed in human brain tissues of Alzheimer patients. Dominant negative mutants derived from the RTK act as tyrosine kinase modulators. The sequence is used to identify compounds that modulate biological and/or pharmacological activity of tyrosine kinase and hence regulate cellular and tissue physiology. The present sequence and the modulators of tyrosine kinase are used for treating many diseases related to or mediated by RTK e.g. adenocarcinoma, angiogenesis, arthritis, diabetic retinopathy, ischemic heart disease, atherosclerosis, inflammation, solid tumours and metastases

SQ

Sequence 422 AA;

Query Match Score 2192; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 8 2e-215;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGMTMLLECSLSDPKLCLVQEKYEVILVPTPLTVTFLILLGVLWLFIREQRTQQRSQ 60
DQ 1 MGMTMLLECSLSDKLCLVQEKYEVILVPTPLTVTFLILLGVLWLFIREQRTQQRSQ 60
QY 61 PGGTAPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 120
DQ 61 PGGTAPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 120
QY 121 CGSGCGPPIFANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 180
DQ 121 CGSGCGPPIFANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 180
QY 181 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 240
DQ 181 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 240
QY 241 FLQEKHLFFGDVAARNILIMOSDITAKLJCGJGLAYEVYTRGAISSTOTIPKWLAPERLIL 300
DQ 241 FLQEKHLFFGDVAARNILIMOSDITAKLJCGJGLAYEVYTRGAISSTOTIPKWLAPERLIL 300

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Db Sequence 495 AA;

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QY 301 RPASIRADWNSFGILLYEMTMLGAPPYPEVPTSLIEHLQRKIMKRPSSCTHTMYSINK 360
DQ 301 RPASIRADWNSFGILLYEMTMLGAPPYPEVPTSLIEHLQRKIMKRPSSCTHTMYSINK 360
QY 361 SCWRWREADRSPRELRLEAAIKTADEAVLQVPELYAVAGIRVESLYNYS 420
DQ 361 SCWRWREADRSPRELRLEAAIKTADEAVLQVPELYAVAGIRVESLYNYS 420
QY 421 ML 422
DQ 421 ML 422

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RESULT 2
ID AAB65706 standard; protein; 495 AA.
AC AAB65706;
XX 27-MAR-2001 (first entry)
DE Novel protein kinase, SEQ ID NO: 235.
XX Human; mouse; protein kinase; antiarthritic; antischlerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;

KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX Homo sapiens.
XX WO200073469-A2.
XX PD 07-DEC-2000.
XX PP 26-MAY-2000; 2000WO-US014842.
XX PR 28-MAY-1999;
XX PA (SUGE-) SUGEN INC.
XX PT Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX WPI; 2001-032161/04.
DR N-PSDB; AAP44735.
XX PR Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.

XX Claim 10; Fig 1; 310pp; English.

XX The present sequence is a novel protein kinase. The novel protein kinases CC and the nucleic acids that encode them may be used in the treatment and CC diagnosis of diseases associated with inappropriate kinase expression CC such as immune-related diseases and disorders, cardiovascular disease, CC neurodegenerative diseases and/or cancers. The nucleic acids and CC complementary sequences may also be used as DNA probes in diagnostic CC assays. The kinase polypeptides may be used as antigens in the production CC of antibodies of kinase expression and activity. Anti-kinase antibodies CC and kinase antagonists may also be used to down regulate kinase CC expression and activity. Diseases related to kinase expression and CC activity include rheumatoid arthritis, atherosclerosis, autoimmune CC disorders, complications of organ transplantation, myocardial infarction, CC immune disorders, cardiomopathies, strokes, renal failure, oxidative- CC stress related disorders, chronic inflammatory bowel disease, chronic CC psoriasis, rhinitis, multiple sclerosis, asthma, osteoarthritis, CC disorders
XX SQ Query Match Score 2192; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 1e-214;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGMTMLLECSLSDKLCLVQEKYEVILVPTPLTVTFLILLGVLWLFIREQRTQQRSQ 60
DQ 1 MGMTMLLECSLSDKLCLVQEKYEVILVPTPLTVTFLILLGVLWLFIREQRTQQRSQ 60
QY 61 PGGTAPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 120
DQ 61 PGGTAPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 120
QY 121 CGSGCGPPIFANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 180
DQ 121 CGSGCGPPIFANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 180
QY 181 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 240
DQ 181 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 240
QY 241 FLQEKHLFFGDVAARNILIMOSDITAKLJCGJGLAYEVYTRGAISSTOTIPKWLAPERLIL 300
DQ 241 FLQEKHLFFGDVAARNILIMOSDITAKLJCGJGLAYEVYTRGAISSTOTIPKWLAPERLIL 300

QY 301 RPASIRADWNSFGILLYEMTMLGAPPYPEVPTSLIEHLQRKIMKRPSSCTHTMYSINK 360
DQ 301 RPASIRADWNSFGILLYEMTMLGAPPYPEVPTSLIEHLQRKIMKRPSSCTHTMYSINK 360
QY 361 SCWRWREADRSPRELRLEAAIKTADEAVLQVPELYAVAGIRVESLYNYS 420
DQ 361 SCWRWREADRSPRELRLEAAIKTADEAVLQVPELYAVAGIRVESLYNYS 420
QY 421 ML 422
DQ 421 ML 422

Db 121 CGSGCGPPIFRANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 180
Db 194 CGSGCGPPIFRANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 253
QY 61 PGGTAPVPPRDLSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 120
Db 74 MGMTMLLECSLSDKLCLVQEKYEVILVPTPLTVTFLILLGVLWLFIREQRTQQRSQ 60
QY 134 PGQIAEVPPPRDLSSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 193
Db 134 PGQIAEVPPPRDLSSWEAGGGNVALPLKETSVENFLGATTPALAKLQVPREQSEVLFQI 193
QY 121 CGSGCGPPIFRANMNTGDPSPKSVTKLAKKEPAQHHEVDFLGLPITOFLGKHNLYQL 180
Db 181 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 240
QY 181 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 240
Db 254 EGCCTEKLPLYMLVEDVAQGDLGLFIWTCCRDMTMGMDGLYDLTKEQYTHIGKQVLLAE 313
QY 241 FLQEKHLFFGDVAARNILIMOSDITAKLJCGJGLAYEVYTRGAISSTOTIPKWLAPERLIL 300
Db 314 FLQEKHLFFGDVAARNILIMOSDITAKLJCGJGLAYEVYTRGAISSTOTIPKWLAPERLIL 373
QY 301 RPASIRADWNSFGILLYEMTMLGAPPYPEVPTSLIEHLQRKIMKRPSSCTHTMYSINK 360
Db 374 RPASIRADWNSFGILLYEMTMLGAPPYPEVPTSLIEHLQRKIMKRPSSCTHTMYSINK 433

Page 3

DR WPI: 2001-626432/72.
DR N-PSDB; AA559829.

XX New polypeptides and nucleic acids, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone degenerative disorders, cancer and promoting wound healing.

PT PT XX

PT XX

PT XX

XX Claim 20; Page 261; 33pp; English.

XX The invention relates to isolated human polypeptides (which may be cytokins) and the polymucleotides encoding them. The protein is useful for identifying a compound which binds to it (e.g. modulators, agonists and antagonists). The polymucleotides are useful as an array for mismatch detection. The proteins and nucleic acids are useful as nutritional sources or supplements. The protein exhibits activity relating to cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity, immune stimulating or immune suppressing and activating or inhibiting related activities. The proteins (and antibodies raised against them) and nucleic acids are therefore useful in the diagnosis and treatment of diseases and disorders such as cancer, central and peripheral nervous system diseases and neuropathies, Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders, thrombocytopenia, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence represents a novel protein of the invention.

XX Sequence 458 AA;

Query Match 99.8%; Score 2186; DB 4; Length 458;
Best Local Similarity 99.8%; Pred. No. 2.4e-214; Indels 0; Gaps 0;
Matches 421; Conservative 1; Mismatches 0;

Db 37 MGMTMLLESLDKLVCIVQEKOEVIVIPTLVITLFLGVILWLFIREQRTQQRSQ 96

Qy 61 PQGIAFPVPPRDLSSWEAGHGNVALPLKETSVENFLGATPALKLQVPREQSEVLEQI 120

Db 97 PQGIAFPVPPRDLSSWEAGHGNVALPLKETSVENFLGATPALKLQVPREQSEVLEQI 156

Qy 121 CGSGCGP1FRANMNTGDPSPKPSVSKVLLKALKEPAGLHEVQDFLGR1QFHQYLGKHNVLQ 180

Db 157 CGSGCGP1FRANMNTGDPSPKPSVSKVLLKALKEPAGLHEVQDFLGR1QFHQYLGKHNVLQ 216

Qy 181 EGCCCTKPLPLMVLVEDAQGLIGFTWCRDYMMDGLYDLTEKQVTHIGKVLLALE 240

Db 217 EGCCCTEKLPLPLMVLVEDAQGLIGFTWCRDYMMDGLYDLTEKQVYHIGKVLLALE 276

Qy 241 FLQEKHIFHGDIVAARNILMQSDLTAKICGLGLAYEVTGRAGISSTOTIPKLWPLERLLL 300

Db 277 FLQEKHIFHGDIVAARNILMQSDLTAKICGLGLAYEVTGRAGISSTOTIPKLWPLERLLL 336

Qy 301 RPASTRADWSEGILLYEMVTLGAPPVEPPTSLIEHLQRKIMRPSSTCITHMYSIMK 360

Db 337 RPASTRADWSEGILLYEMVTLGAPPVEPPTSLIEHLQRKIMRPSSTCITHMYSIMK 396

Qy 361 SCWRWREADRSPREPLRLERAAIKTADDEAVLQVPELVEPELYAAVAGIRVESLYNYS 420

Db 397 SCWRWREADRSPREPLRLERAAIKTADDEAVLQVPELVEPELYAAVAGIRVESLYNYS 456

Qy 421 ML 422
Db 457 ML 458

XX AAG66404 standard; protein; 422 AA.

XX AAG66404;
XX DT 17-OCT-2001 (first entry)

XX DE Human fibrous growth factor receptor 46.

XX KW Human; fibrous growth factor receptor 46; cancer; HIV infection; KW cytostatic; anti-HIV.

XX OS Homo sapiens.

XX PN CN1296965-A.

XX PD 30-MAY-2001.

XX PF 23-NOV-1999; 99CN-00124072.

XX PR 23-NOV-1999; 99CN-00124072.

XX PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.

XX PI Mao Y, Xie Y;

XX DR; 2001-483896/53.

XX N-PSDB; AAH75803.

XX Polypeptide-human fibrous growth factor receptor 46 and polynucleotide for coding said polypeptide.

PS Claim 1; Page 22-23 (Disclosure); 29pp; Chinese.

XX The present sequence is the protein sequence for human fibrous growth factor receptor 46. The receptor and its coding sequence are useful in the treatment of diseases e.g. cancer and HIV infection.

XX SQ Sequence 422 AA;

Query Match 99.6%; Score 2183; DB 4; Length 422;
Best Local Similarity 99.5%; Pred. No. 6.8e-214; Indels 0; Gaps 0;
Matches 420; Conservative 1; Mismatches 1;

Qy 1 MGMTMLLESLDKLVCIVQEKOEVIVIPTLVITLFLGVILWLFIREQRTQQRSQ 60

Db 1 MGMTMLLESLDKLVCIVQEKOEVIVIPTLVITLFLGVILWLFIREQRTQQRSQ 60

Qy 61 PQGIAFPVPPRDLSSWEAGHGNVALPLKETSVENFLGATPALKLQVPREQSEVLEQI 120

Db 61 PQGIAFPVPPRDLSSWEAGHGNVALPLKETSVENFLGATPALKLQVPREQSEVLEQI 156

Qy 121 CGSGCGP1FRANMNTGDPSPKPSVSKVLLKALKEPAGLHEVQDFLGR1QFHQYLGKHNVLQ 180

Db 121 CGSGCGP1FRANMNTGDPSPKPSVSKVLLKALKEPAGLHEVQDFLGR1QFHQYLGKHNVLQ 180

Qy 181 EGCCCTEKLPLPLMVLVEDAQGLIGFTWCRDYMMDGLYDLTEKQVTHIGKVLLALE 240

Db 181 EGCCCTEKLPLPLMVLVEDAQGLIGFTWCRDYMMDGLYDLTEKQVYHIGKVLLALE 240

Qy 241 FLQEKHIFHGDIVAARNILMQSDLTAKICGLGLAYEVTGRAGISSTOTIPKLWPLERLLL 300

Db 241 FLQEKHIFHGDIVAARNILMQSDLTAKICGLGLAYEVTGRAGISSTOTIPKLWPLERLLL 336

Qy 300 RPASTRADWSEGILLYEMVTLGAPPVEPPTSLIEHLQRKIMRPSSTCITHMYSIMK 360

Db 300 RPASTRADWSEGILLYEMVTLGAPPVEPPTSLIEHLQRKIMRPSSTCITHMYSIMK 396

Qy 361 SCWRWREADRSPREPLRLERAAIKTADDEAVLQVPELVEPELYAAVAGIRVESLYNYS 420

Db 397 SCWRWREADRSPREPLRLERAAIKTADDEAVLQVPELVEPELYAAVAGIRVESLYNYS 456

QY 361 SCWRWREADRSPSPRELRLLEAIKTADEAVLQVPELVPELYAAVAGIRVESLFNTYS 420
 Db 361 SCWRWREADRSPSPRELRLLEAIKTADEAVLQVPELVPELYAAVAGIRVESLFNTYS 420

QY 421 ML 422
 Db 421 ML 422

RESULT 6
 AAY44298 standard; protein; 421 AA.
 XX DT 29-FEB-2000 (first entry)
 XX DE Human receptor tyrosine kinase dominant negative mutant -1.
 XX KW Human; receptor tyrosine kinase; RTK; tyrosine kinase modulator;
 KW signal transduction tyrosine kinase; tumour; dominant negative mutant;
 KW cancer; adenocarcinoma; Rtk associated disorder; adenocarcinoma;
 KW angiogenesis; arthritis; diabetes; diabetic retinopathy; ischaemic heart disease;
 KW atherosclerosis; inflammation.
 XX OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 146..147 /note= "Wild type Lys at position 147 is deleted"
 XX PN WO9954589-A1.
 XX PD 16-DEC-1999.
 XX PF 08-JUN-1999; 99WO-GB001798.
 XX PR 11-JUN-1998; 98US-0088958P.
 XX PA (ZENE) ZENECA LTD.
 XX PT Ghidyal N, Panchamoorthy G;
 XX DR 2000-097538/08.
 XX PT New nucleic acid encoding human tyrosine kinase, overexpressed in, e.g.
 XX cancers For treating adenocarcinoma.
 XX Claim 3; Page: 56pp; English.

XX The present sequence is a dominant negative mutant of human receptor tyrosine kinase (RTK), which is obtained by deleting Lys at position 147 of wild type sequence. The mutant modulates biological and/or pharmacological activity of tyrosine kinase and hence regulates cellular and tissue physiology. The present sequence is used for treating many diseases related to or mediated by RTK e.g. adenocarcinomas, angiogenesis, arthritis, diabetic retinopathy, ischaemic heart disease, atherosclerosis, inflammation, solid tumours and metastases. Note: The present sequence is not given in the specification but has been derived from SEQ ID NO: 3 given in Sequence Listing

XX SQ Sequence 421 AA;

Query Match 99.3%; Score 2176.5; DB 3; Length 421;
 Best Local Similarity 99.8%; Pred. No. 3.1e-213;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGMTMLLSESLDULCVIQEKQYVITYVTLVITFLILGTVLWFIREQTOQQSG 60
 Db 1 MGMTMLLSESLDULCVIQEKQYEVIVVTPLLVTIRLFLGVILWFIREQTOQQSG 60

QY 61 POGTAPVPDPPLKETSVENFLGATTTPALAKLQVPREOLSEVLEQI 120
 Db 61 PQGATPVPPDLSWEAHHGGNVALPKETSVENFLGATTTPALAKLQVPREOLSEVLEQI 120

QY 121 CGSGCGPIFRANNNTGDPSPKPSKVILKALKEPGLHEVQDFLGIQFQYLGKHNLYQL 180
 Db 121 CGSGCGPIFRANNNTGDPSPKPSKVIL-ALKEPGLHEVQDFLGIQFQYLGKHNLYQL 179

QY 181 EGCTCTKPLVWLEDAQGDLLGFMTCRDWTMDGLYDTEKQVHIGKQVIALE 240
 Db 180 EGCTCTKPLVWLEDAQGDLLGFMTCRDWTMDGLYDTEKQVHIGKQVIALE 300

QY 241 FLOEKHLFHGDVAARNTIMOSDITAKLGLGLAYEVTRGAISSTOTIPLKMLAPERLLL 299
 Db 240 FLOEKHLFHGDVAARNTIMOSDITAKLGLGLAYEVTRGAISSTOTIPLKMLAPERLLL 299

QY 301 RPASIRADWVSPFGILYEMVTLGAPPKPEVPPTSILEHLQRKIMKRPSSTHTMYSIMK 360
 Db 300 RPASIRADWVSPFGILYEMVTLGAPPKPEVPPTSILEHLQRKIMKRPSSTHTMYSIMK 359

QY 361 SCWRWREADRSPREPLRLEAAIKTADDEAVLQVPLVWPELYAAVAGIVESLYNNYS 420
 Db 360 SCWRWREADRSPREPLRLEAAIKTADDEAVLQVPLVWPELYAAVAGIVESLYNNYS 419

QY 421 ML 422
 Db 420 ML 421

RESULT 7
 AAB66603 standard; protein; 209 AA.
 XX ID AAB66603
 AC AAB66603;
 XX DT 04-APR-2001 (first entry)
 XX DE Human h14833 protein.
 XX KW Human; protein kinase; cell growth; tumour; cancer; immune; inflammatory;
 KW respiratory; haematological; bone disorder.
 XX OS Homo sapiens.
 PN WO200100879-A1.
 XX PD 04-JAN-2001.
 XX PP 30-JUN-2000; 2000WO-US018291.
 XX PR 30-JUN-1999; 99US-00345473.
 XX PR 01-MAY-2000; 2000US-00562480.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Hodge MR, Meyers R, Williamson M;
 DR WPI; 2001-06197/07.
 XX PT New protein kinase polypeptides, nucleic acids and anti-kinase antibodies, useful for diagnosing and treating e.g. cancer, inflammatory, immune, cardiovascular and bone disorders.
 XX PS Claim 1; Fig 7; 93pp; English.

XX The present invention relates to human protein kinase. The proteins are from new human genes termed h12832, h14138, h4833, h15930, h15993, h1634 and h2252. The proteins may be used to identify modulators of their activity. The proteins may also be used to derive products for the treatment of cellular growth related disorders, malignancies, cancers, immune, inflammatory, respiratory, haematological and bone-related disorders.

XX Ruben SM, Shi Y, Young PE, Ni J;
 XX WPI; 2001-296976/30.
 DR N-PSDB; AAD3998.

XX New isolated nucleic acid molecule for producing human protein tyrosine kinase receptor.

XX PT
 PT (MOLE-) MOLECULAR DYNAMICS INC.

PS Claim 12; Page 283; 288pp; English.

XX The present sequence is human protein tyrosine kinase receptor (PTK) from clone HAGB04. The invention relates to human protein tyrosine kinase (PTK) receptors and their corresponding cDNA molecules. PTK receptors are useful in providing immunological probes for differential identification of the tissues or cell types present in a biological sample. PTK is used in methods for the diagnosis, prevention and treatment of various disorders related to PTK such as immune system disorders (severe combined immunodeficiency (SCID); hyperproliferative disorders (neoplasm, sarcoidosis; central nervous system disorders (multiple sclerosis), atherosclerosis); cardiovascular disorders (arrhythmia, neurodegenerative disorders (Alzheimer's disease, Parkinson's disease); blood coagulation disorders (thrombocytopaenia); autoimmune disorders (biliary cirrhosis, Crohn's disease); respiratory disorders (asthma, allergy); gastrointestinal disorders (inflammatory bowel disease); cerebrovascular disorders (stroke); vascular dementia); brain disorders (phenylketonuria); cancers (such as ovarian, lung, bladder, liver, breast and lymphomas); behavioural disorders ('Tourette's syndrome') and musculo-skeletal disorders (arthritis, trauma, tendonitis; renal disorders (nephrotic syndrome, Glomerulonephritis); metastases of malignancies and related disorders (leukaemia, multiple myeloma); and infections caused by bacteria, viruses, fungi and parasites. PTK is also useful for screening therapeutic compounds. PTK is used as an antigen in a vaccine to raise an immune response against infectious disease. PTK nucleic acids are useful in gene therapy.

XX Sequence 104 AA;

Query Match 24.7%; Score 542; DB 4; Length 104;
 Best Local Similarity 100.0%; Pred. No. 4.8e-47;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db ID 319 MVTLGAPPVPPPTILEHQLRCKIMKRPSSCTHTMYSIMKSCKMRWREADRSPRELU 378
 AC 1 MVTLGAPPVPPPTILEHQLRCKIMKRPSSCTHTMYSIMKSCKMRWREADRSPRELU 60

Qy 379 RLEAAIKAIIKTDDEAVLQVPELVPELYAAVAGIRVESSLFYNNYSML 422
 Db 61 RLEAAIKAIIKTDDEAVLQVPELVPELYAAVAGIRVESSLFYNNYSML 104

RESULT 1.0
 ABB3239 standard; peptide; 93 AA.
 AC ABB3239
 XX DT 04-FEB-2002 (first entry)
 DE Peptide #10745 encoded by human foetal liver single exon probe.
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 OS Homo sapiens.
 XX DT 09-AUG-2001 (first entry)
 PR WO200157277-A2.
 PN WO200157277-A2.
 XX PD 09-AUG-2001.
 PR 30-JAN-2001; 2001WO-US000663.
 XX PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608400.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

PR 30-JUN-2000; 2000US-00608400.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA Penn SG, Hanzei DK, Chen W, Rank DR;
 XX PR WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.

XX PS Claim 27; SEQ ID NO 35874; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human fetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 93 AA;

Query Match 20.6%; Score 452; DB 4; Length 93;
 Best Local Similarity 100.0%; Pred. No. 6.4e-38;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 IAPVPPRDLSWEAGGGNVALPLKTSVNLFLGATTPALAKLQVPREQSEVLBICSG 123
 Db 1 IAPVPPRDLSWEAGGGNVALPLKTSVNLFLGATTPALAKLQVPREQSEVLBICSG 60

XX SQ Sequence 93 AA;

Query Match 20.6%; Score 452; DB 4; Length 93;
 Best Local Similarity 100.0%; Pred. No. 6.4e-38;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 SCGPPIFRANNNTGDPSPKPSVILALK 150
 Db 61 SCGPPIFRANNNTGDPSPKPSVILALK 87

RESULT 11
 AAM37079
 ID AAM37079 standard; protein; 93 AA.
 AC AAM37079;
 XX DT 17-OCT-2001 (first entry)
 DB Peptide #11116 encoded by probe for measuring placental gene expression.
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX OS Homo sapiens.
 PN WO200157272-A2.

XX PD 09-AUG-2001.
 PR 30-JAN-2001; 2001WO-US000663.

XX PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608400.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

PR Penn SG, Hanzei DK, Chen W, Rank DR;

PI

XX	WPI; 2001-4B8897/53.
XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
XX	Claim 27: SEQ ID NO 37348; 654pp; English.
XX	The present invention relates to single exon nucleic acid probes (SENP; see AA131315 AA151546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
XX	Sequence 93 AA;
XX	Query Match 20.6%; Score 452; DB 4; Length 93; Best Local Similarity 100.0%; Pred. No. 6.4e-38; Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	QY 64 IAPPVPPRDLISMEGHGGNVALPKETSVENFLGATTPLAKLQVPRQLSEVLEQTCG 123 Db 1 IAPPVPPRDLISMEGHGGNVALPKETSVENFLGATTPLAKLQVPRQLSEVLEQTCG 60
XX	QY 124 SCGP1FRAANNNTGDESKPKSVILKALK 150 Db 61 SCGP1FRAANNNTGDESKPKSVILKALK 87
XX	RESULT 12 AAM76972 standard; protein; 93 AA. ID AAM76972 XX AC AAC XX DT 06-NOV-2001 (first entry) XX Human bone marrow expressed probe encoded protein SEQ ID NO: 37278. XX KW Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma. XX Homo sapiens. XX WO200157276-A2. XX PD 09-AUG-2001. XX PF 30-JAN-2001; 2001WO-US000668. XX PR 04-FEB-2000; 2000US-0180312P. PR 26-MAY-2000; 2000US-0207456P. PR 30-JUN-2000; 2000US-00609408. PR 03-AUG-2000; 2000US-0064366P. PR 21-SEP-2000; 2000US-0234687P. PR 27-SEP-2000; 2000US-0236359P. PR 04-OCT-2000; 2000GB-00024263. XX PA (MOLE-) MOLECULAR DYNAMICS INC. XX PI Penn SG, Hanzel DK, Chen W, Rank DR; XX DR WPI; 2001-4B88900/53.
XX	Example 4; SEQ ID NO 37278; 658pp + Sequence Listing; English.
XX	The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a CC protein encoded by one of the probes of the invention
CC Sequence 93 AA:
XX SO

Claim 27: SEQ ID NO 37348; 654pp; English.

The present invention relates to single exon nucleic acid probes (SNPs; see AAT1315-AA15746). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

Sequence 93 AA;
 124 SCGPFRANNNTGDSKPKSEVYLKALK 87
 61 SCGPFRANNNTGDSKPKSEVYLKALK 87

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Query Match          Score 452; DB 4; Length 93;
Doc. Local similarity 100.0%; Dred No 6 4e-38;
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 64 TAPVDPPIITSWRAGHGGNVAIPIKETTSVENVELGATTPLAKLOVPREOLSEVIEQICSG 123
 best local 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 87; Insertions 0; Deletions 0; Gaps 0;
 RESULT 13
 ID AAM61146
 65 TAPVDPPIITSWRAGHGGNVAIPIKETTSVENVELGATTPLAKLOVPREOLSEVIEQICSG 123
 best local 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 87; Insertions 0; Deletions 0; Gaps 0;
 RESULT 13
 ID AAM61146 standard; protein; 93 AA.

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Human brain expressed single exon probe encoded protein SEQ ID NO: 36251.
 05-Nov-2001 (first entry)
 XX
 xx
 xx

RESULT 12
Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

Human bone marrow expressed probe encoded protein SEQ ID NO: 37778.
 Human bone marrow expressed exon: gene expression analysis: probe:
 DE XX
 PF XX
 PR 04-FEB-2000; 2000US-US000567.
 PR 30-JAN-2001; 2001WO-US000567.

RW	<i>microarray</i> ; <i>cancer</i> ; <i>leukaemia</i> ; <i>lymphoma</i> ; <i>myeloma</i> .	2000US-020745P.	PR
XX		2000US-00608408.	PR
		2000US-00632466.	PR
		2000US-00632466.	PR
	<i>Homo sapiens</i> .		

PR 21-SEP-2000 ; 2000US-123468-JP.
PR 27-SEP-2000 ; 2000US-023635JP.
PR 04-OCT-2000 ; 2000GB-0002463.
PR WO200157276-A2 .
XX XX

XX F-1 REUNION, MARSHAL LAW, CIVILIAN, COMMUNIST
XX XX DR WPI; 2001-483446/52.
XX

Single exon nucleic acid probes for analyzing gene expression in human brains.

The present invention provides a number of single exon nucleic acid molecules.

Penn SG, Hanzel DK, Chen W, Rank DR; *CC probes which are derived from genomic sequences expressed in brain cell samples, CC brain. They can be used to measure gene expression in brain cell samples, CC which may enable the diagnosis and improved treatment of nervous system CC disorders.*

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention

PT gene expression in human bone marrow.
XX Sequence 93 AA;
SQ DQ047396
DB 4;
Length 93;

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human marrow. The present invention also provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain.

Qy	64	IAPVPPRDLSEWAHGCGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLEQICSG	123
Db	1	IAPVPPRDLSEWAHGCGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVLEQICSG	60
Qy	124	SCGPPIFRANNMTGDPSPKPKSVTILKALK	150
Db	61	SCGPPIFRANNMTGDPSPKPKSVTILKALK	87
RESULT 14			
	ABG5833		
ID	ABG5833	standard; peptide;	93 AA.
XX			
AC	ABG5833;		
XX			
DT	25-FEB-2003	(first entry)	
XX			
DE	Human liver peptide, SEQ ID No 37281.		
XX			
KW	Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;		
KW	hypercholesterolaemia; coronary heart disease.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157273-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	30-JAN-2001; 2001WO-US000664.		
XX			
PR	04-FEB-2000; 2000US-018312P.		
PR	26-MAY-2000; 2000US-0207456P.		
PR	30-JUN-2000; 2000US-0207456P.		
PR	03-AUG-2000; 2000US-00632366.		
PR	21-SEP-2000; 2000US-0234687P.		
PR	27-SEP-2000; 2000US-0234687P.		
PR	04-OCT-2000; 2000US-0232359P.		
PR	2000GB-00024263.		
PA	(MOLE-) MOLECULAR DYNAMICS INC.		
XX			
PI	Penn SG, Hanzel DK, Chen W, Rank DR;		
XX			
DR	WPI; 2001-488898/53.		
PT	Human genome-derived single exon nucleic acid probes useful for analyzing		
XX	gene expression in human adult liver.		
PS	Claim 27: SEQ ID NO 37281; 658PP; English.		
XX			
CC	The invention relates to a single exon nucleic acid probe (SENP) (I) for		
CC	measuring human gene expression in a sample derived from human adult		
CC	liver, comprising one of 13109 defined nucleotide sequences given in the		
CC	specification (or complements/ fragments). The probe hybridises at high		
CC	stringency to a nucleic acid molecule expressed in the human adult liver.		
CC	in samples derived from human adult liver. The genes identified may be		
CC	involved in genetic liver diseases such as <i>cirrhosis</i> ,		
CC	hyperlipoproteinemia, hyperlipidemia and hypercholesterolemia which is		
CC	associated with coronary heart disease. ABG47348-ABG5930 represent human		
CC	liver single exon encoded peptides of the invention. Note: The sequence		
CC	information for this patent does not appear in the printed specification		
CC	but was obtained in electronic form directly from WIPO at		
CC	ftp.wipo.int/pub/mblncluded/not		

Query	Match	20.3%	Score	444;	DB	4;	Length	801;
Best Local	Similarity	30.5%	Pred. No.	1e-35;				
Matches	120;	Conservative	Mismatches	165;	Indels	38;	Gaps	10;
2y	34	VTIFLILGVILWLFIREQTTOQQRSQPGQIAPV--PPPRDLKSEAGHGCGNVALPLKET	90					
Dy	375	VFFFLFILVVAVILCRLSPKKLGSPVTHKVYSRFLPKRQVLEESNSMNSNTPL--V	432					
Dy	91	SVENFLGATTPALA--KLQVP-----REPSVELEQIGSGCPIFRAMMTGTD	137					
	:	: : : : : : : : : : : : : : : : : : : : : : : :	.					

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Page 10

Db 433 RIARLSSGEGPVLANYSELELPADPKWELSRTRLTGKPLGEGCFGQVYMAEAIGIDKDR 492
Qy 138 PSKPKEVILKALKEPGLHKEYQDFLGRIQPHOYLGRHKNLYQLEGCTEKLPLIMLVEDV 197
Db 493 TAKPVTVAVRMKDDATDKDUSDVSEMENMMKGKHNIINLLGACTGGPLYVVEYA 552
Qy 198 AQGDILGFILWTCRDRDMTMGILY-----DLTEKOVYTHIGKQVIALEFLQEKLH 247
Db 553 AKGNLREFL-PARRP---PGNDYSPACRIPEEQUTCDLVSACAQVARGELEYLASQKC 607
Qy 248 FHGDVAARNILMOSDITAKLCGLAYEVYTRGAISSTQ--IPLKWLAPERLLRPASI 305
Db 608 IHRDLAARNVLVITEDNYMKIADEGLARDVHNLDYKKTNGRLPVKMAPAEALFEDVTH 667
Qy 306 RADVWSPPOTLLYEMVTGAP-DPEPEVPTSILEHLQRKIMRKPSSTHTMXSIMKSCWR 364
Db 668 QSDVWSFCEVLLWEIFTPGSPSPYGPIVWEELKLKEGRMDKPASTDHYMINRECWHD 727
Qy 365 WREADRPSPRELRRLRLE-AAIKTADDEAVLOYP 396
Db 728 AVBSQRPFPEKQLVEDLDRLLTVTSTDYLIDLSDVP 761

Search completed: June 14, 2004, 18:44:17
Job time : 61 secs

Gencore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 protein - protein search, using sw model
 on: June 14, 2004, 18:41:39 ; Search time 45 Seconds
 (without alignments)
 2958.860 Million cell updates/sec
 title: US-10-040-884-3
 perfect score: 2192
 sequence: 1 MGMTMLLECSLSDKLCVQI.....LYAAVAGIRVESLFYNSML 422
 scoring table: BL0SUM62
 Gapext 10.0 , Gapext 0.5
 searched: 1017041 seqs, 315518202 residues
 - al number of hits satisfying chosen parameters: 1017041
 minimum DB seq length: 0
 maximum DB seq length: 2000000000
 post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 database : OBNE85

ALIGNMENTS						
RESULT 1						
OONSHI						
2:	sp_bacteria:*					
3:	sp_fungi:*					
4:	sp_human:*					
5:	sp_invertebrate:*					
6:	sp_mammal:*					
7:	sp_mhc:*					
8:	sp_organelle:*					
9:	sp_phage:*					
10:	sp_plant:*					
11:	sp_rabbit:*					
12:	sp_rat:*					
13:	sp_vertebrate:*					
14:	sp_unclassified:*					
15:	sp_rvirus:*					
16:	sp_bacteriaph:*					
17:	sp_archeap:*					
SEQUENCE FROM N.A.						
RC	SEQUENCE=Amygdala;					
RA	Blum H., Bauersachs S., Newes H.W., Weil B., Wiemann S.;					
RL	Submitted (APR-2000) to the EMBL/GenBank/DDJB databases.					
DR	EMBL; AL353940; CAB892501; - .					
DR	PIR; T48680; T48680.					
HSSP	P08631; IADS.					
DR	GO; GO-0005524; F:ATP binding; IEA.					
DR	GO; GO-0004713; F:protein-tyrosine kinase activity; IEA.					
DR	GO; GO-0016740; F:transferrase activity; IEA.					
DR	GO; GO-0006468; P:protein amino acid phosphorylation; IEA.					
DR	InterPro; IPR00719; Prot kinase.					
DR	InterPro; IPR001245; Tyr_Pkinase.					
DR	InterPro; IPR0069; pkinase; I.					
DR	PFAM; PF00069; pkinase_AS.					
DR	PRINTS; PR00105; TYRKINASE.					
DR	ProDom; PD00001; Prot kinase.					
DR	ProSITE; PS50011; PROTEIN KINASE_DCM; 1.					
DR	ProSITE; PS00109; PROTEIN_KINASE_TYR; 1.					
KW	Hypothetical protein; ATP-binding; Kinase.					
KW	Tyrosine-protein kinase.					
SQ	SEQUENCE 422 AA; 47546 MW;					
Query Match	100.0%					
Boot. Match Similit.	100.0%					
DB 4	Score: 2192;					
Length	422;					

SQ	SEQUENCE	429 AA;	48121 MW;	480130D319551F61 CRC64;	
Query Match Similarity 76.8%; Score 1684.5; DB 11; Length 429; Best Local Matches 37; Mismatches 55; Indels 3; Gaps 2;					
Qy	3	GTAPVPPRDLWS-EAGHGNVALPLKETSVENFLGATTPALAKLQYPREQLESEVLEQIC 62		DR Prodrom; PD000001; Prot kinase; 1.	
Db	7	LSRVILLECSLSDKLXCVREKQEVIVIVALLYGFLLILWLFGRQRSGPQ 66		DR SMART; SM00220; S_TKc; 1.	
Qy	63	GIAFPVPPRDLWS-EAGHGNVALPLKETSVENFLGATTPALAKLQYPREQLESEVLEQIC 121		DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.	
Db	67	GTASVPASRGRSQAAGHEGEKYLPLKETSVENFLGATTPALAKLQYPREQLESEVLEQIC 126		DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.	
Qy	122	SSCGCP1FRANNNTGDSKPKSVYIKALKKEPLGLHEVQDFLGRIQFFQYQGLKHNLYQLE 181		SEQUENCE 340 AA; 55741BD17DAB256 CRC64;	
Db	127	SGSGCTLYIHYATMTTKDHPKPSVYIKALKKEPLGLHEVQDFLGRIQFFQYQGLKHNLYQLE 186			
Qy	182	GCCTEKULPLMVKLEDVAQGDLLGFLWTCRDWTMDGLYDLTEKQVHIGKQVIALLEF 241		Query Match 61.9%; Score 1357; DB 11; Length 340; Best Local Matches 63.3%; Pred. No. 2. 9e-12; Mismatches 33; Indels 90; Gaps 2;	
Db	187	GCCTERPLPLMVKLEDVAQGDLLGFLWTCRDWTMDGLYDLTEKQVHIGKQVIALLEF 246			
Qy	242	IQEKHLFHGDAARNILMQSDLTAKLICGLGLAYENVTRGAIS--TQTIPLKWLAPERLL 299		3 MTRMLIEBCSLSPDKLCVQEKQYEVIIVPTLYTIVLFLGTVLWLFIREQTOQQSGPQ 62	
Db	247	IQEKHLFHGDAARNILMQSDLTAKLICGLGLAYENVTRGAIS--TQTIPLKWLAPERLL 306		7 LSRLVILCSSLSPDKLCVREKQYEVIIVLPALLYGGFLILAILWLFTRGQSRQSGP- 65	
Qy	300	LRPASTRADWNSFGLLYEMYLGAPPVNPPTSLLEHQLRKIMKRPSSCTHTMYSIM 359			
Db	307	LRPASTRGDTWSFGLLYEMYLGAPPVNPPTSLIQYLORKIMKRPSSCTSHANYNM 366		63 GIAPVPPRDLWS-EAGHGNVALPLKETSVENFLGATTPALAKLQYPREQLEQICS 122	
Qy	360	KSCWRNPREADSPSPRELRLRLEAAIKADDAVLOVPELYTAAVAGTRVESUFYNN 419		Db 66 -----	
Db	367	KCCWRMSEDSRPBLQGQLQRLREAASSADKAVLQPELVPELYADVAGRAEISYSF 426		Qy 123 GSCGP1FRANNNTGDSPKPSVILKALKEPLAGLHEVQDFLGRIQFFQYQGLKHNLYQLEG 182	
Qy	420	SML 422		Db 66 -----	
Db	427	SVL 429		Qy 183 OCTEKULPLMVKLEDVAQGDLLGFLWTCRDWTMDGLYDLTEKQVHIGKQVIALLEF 242	
RESULT 4				Db 99 CCTERPLPLMVKLEDVAQGDLLGFLWTCRDWTMDGLYDLTEKQVHIGKQVIALLEF 158	
Q8BZH6		PRELIMINARY;	PRT;	Qy 243 QEKHLFHGDAARNILQSDLTAKLICGLGLAYENVTRGAIS--TQTIPLKWLAPERLL 300	
AC	Q8BZH6 ;			Db 159 QEKHLFHGDAARNILQSDLTAKLICGLGLAYENVTRGAIS--TQTIPLKWLAPERLL 218	
DT	01-MAR-2003 (TREMBUREL. 23, Created)			Qy 301 RPASITRADWNSFGLLYEMYLGAPPVNPPTSLLEHQLRKIMKRPSSCTHTMYSIM 360	
DT	01-MAR-2003 (TREMBUREL. 23, Last sequence update)			Db 219 RPASITRDWNSFGLLYEMYLGAPPVNPPTSLIQYLORKIMKRPSSCTSHANYNM 278	
DT	01-OCT-2003 (TREMBUREL. 25, Last annotation update)			Qy 361 SCWRNPREADSPSPRELRLRLEAAIKADDAVLOVPELYTAAVAGTRVESUFYNN 420	
DB	Similar to FGF receptor 4B.			Db 279 CCWRNPREADSPSPRELRLRLEAAIKADDAVLOVPELYTAAVAGTRVESUFYNN 420	
GN	A126477			Qy 421 ML 422	
OS	Mus musculus (Mouse).			Db 339 VL 340	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TAXID=10990; [1]				
RN					
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Urinary bladder;				
RX	MEDLINE=2354683; PubMed=12466851;				
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs."				
RL	Nature 420:563-573 (2002).				
DR	EMBL; AK020563; -				
DR	MGD; MG1:2141396; Bac29000.1; -				
DR	GO; GO:0005524; F:ATP binding; IEA.				
DR	GO; GO:004674; F:Protein serine/threonine kinase activity; IEA.				
DR	GO; GO:004713; F:Protein-Tyrosine kinase activity; IEA.				
DR	GO; GO:006468; F:Protein amino acid phosphorylation; IEA.				
DR	InterPro; IPR00719; Prot kinase.				
DR	InterPro; IPR002230; Ser_Ehr_pk kinase.				
DR	InterPro; IPR01245; Tyr_pk kinase.				
DR	InterPro; IPR008266; Tyr_pk kinase_AS.				
DR	PRINTS; PR00109; TYRKINASE.				

DR	GO; GO:0005468; F:protein amino acid phosphorylation; IEA.	DR	EMBL; AB007037; BAA22282.1; -.
DR	GO; GO:0005468; F:protein amino acid phosphorylation; IEA.	DR	PIR; JC4583; JC4583.
DR	InterPro; IPR007110; Ig-like.	DR	HSSP; P1162; 1PGK.
DR	InterPro; IPR003598; Ig_c2.	DR	GO; GO:0005524; F:ATP binding; IEA.
DR	InterPro; IPR000719; Prot_kinase.	DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR	InterPro; IPR001245; Tyr_Pkinase.	DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR008266; Tyr_Pkinase_AS.	DR	GO; GO:0006468; F:transerase activity; IEA.
DR	Pfam; PF00047; Ig; 3.	DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR	Pfam; PF00069; Pkinase; 1.	DR	InterPro; IPR007110; Ig-like.
DR	PRINTS; PRO0109; TYRKINASE.	DR	InterPro; IPR00598; Ig_c2.
DR	Prodrom; PD000001; Prot_kinase; 1.	DR	InterPro; IPR000719; Prot_kinase.
DR	PROSITE; PS00011; PROTEIN_KINASE.	DR	SMART; SM00408; IGC2; 3.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR.	DR	SMART; SM00219; TyrKc; 1.
KW	Tyrosine-protein kinase.	DR	PROSITE; PS00835; IG_LIKE; 3.
KW	Tyrosine-protein kinase.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP.	DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM.	DR	PROSITE; PS00109; PROTEIN_KINASE_TIR; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR.	KW	ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase; ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SEQUENCE	828 AA; 9321 MW;	SEQUENCE	829 AA; 9332 MW; 47463466399BF571 CRC64;
QY	21 EKQEVIVIPTLTVTIFL-IILLGVLMWLFIREQ-RTOQQRSGP--QGIAVPVPPRDLWSW 75	Query Match	21.3%; Score 467.5; DB 13; Length 829;
DB	386 ESRMDILYYT--SGFLAVAMAVIVLICRMOTPSQTQTPVHKLAKPLIOPSL 442	Best Local Similarity	30.1%; Pred. No. 1..3e-32;
QY	76 EAGHHGNVIALPL-KETSVENELGATTPL-----AKLOVPREQSEVL-EQICSGSC 125	Mismatches	84; Mismatches 16;
DB	443 ESSSGKSSAPLRLTRSSCAPMLPGMVEVLPLDAKWEFPRDRL--VLGRKPLGEBCF 500	Indels	37; Gaps 14;
QY	126 GPFTRA--NMNTGDPSPKPSVILKALKEPAQHHEVQDFLGRQFHQYLGRKHKNLVLQLEG 182	Qy	21 EKQEVIVIPTLTVTIFL-IILLGVLMWLFIREQ-RTOQQRSGP--QGIAVPVPPRDLWSW 75
DB	501 GQVTRAEYGIGIEKDRPERPVTAVKMIDNGTDKDLSDISENEMLKVKIGKHKNITNLG 560	Db	387 ESRMDILYYT--SGFLAVAMAVIVLICRMOTPSQTQTPVHKLAKPLIOPSL 443
QY	183 CCTCEKPLPLYMLVEDAQCQDGLFLWTCRDVMMDGLLYDLTE-----KQYHIGKQ 234	Qy	76 EAGHHGNVIALPL-KETSVENELGATTPL-----AKLOVPREQSEVL-EQICSGSC 125
DB	561 VCTOBGPPLVVVEVASKGNREFL-RARRPPTPEDA--FDITRVPEELLSFQLVSCYQ 617	Db	444 ESSSGKSSAPLRLTRSSCAPMLPGMVEVLPLDAKWEFPRDRL--VLGRKPLGEBCF 501
QY	235 VLLALEPLOEKKHLEPASITRADWVSPGILLYEMMTLGAPPYEVPPTSILEHQLRKIMKRPSSCT 352	Qy	126 GPFTRA--NMNTGDPSPKPSVILKALKEPAQHHEVQDFLGRQFHQYLGRKHKNLVLQLEG 182
DB	618 VARGMEYELSKRCRTHDLAARNVLAEDVNMKTADFGILARGVHDIDYXKTKTSNGLPVRW 677	Db	502 GQVTRAEYGIGIEKDRPERPVTAVKMIDNGTDKDLSDISENEMLKVKIGKHKNITNLG 561
QY	293 LAPERLLIPASITRADWVSPGILLYEMMTLGAPPYEVPPTSILEHQLRKIMKRPSSCT 352	Qy	183 CCTCEKPLPLYMLVEDAQCQDGLFLWTCRDVMMDGLLYDLTE-----KQYHIGKQ 234
DB	678 MAPEALDVRVYTHQSDIWSPGCPLVTRFLIGGSPYPGIPEVEELPKLIIEGHRMDKPSNCT 737	Db	562 VCTQEGPLFVVVEVASKGNLREFL-RARRPPTPEDA--FDITRVPEELLSFQLVSCYQ 618
QY	353 HTMYSIMKSCWRWREADRSPRLRLRAAIKTAFFDAV-LQVP 396	Qy	235 VLLALEPLOEKKHLEPASITRADWVSPGILLYEMMTLGAPPYEVPPTSILEHQLRKIMKRPSSCT 352
DB	738 HELYMLRECWHAVPTQRPFKQLVEHLDRLITAVSEYDLSMP 792	Db	619 VARGMEYELSKRCRTHDLAARNVLAEDVNMKTADFGILARGVHDIDYXKTKTSNGLPVRW 678
RESULT 6	Q9PSV8 PRELIMINARY; PRT; 829 AA.	QY	293 LAPERLLIPASITRADWVSPGILLYEMMTLGAPPYEVPPTSILEHQLRKIMKRPSSCT 352
AC	Q9PSV8 PRELIMINARY;	QY	679 MAPEALDVRVYTHQSDIWSPGCPLVTRFLIGGSPYPGIPEVEELPKLIIEGHRMDKPSNCT 738
ID	Q9PSV8 PRELIMINARY;	Db	353 HTMYSIMKSCWRWREADRSPRLRLRAAIKTAFFDAV-LQVP 396
DT	01-MAY-2000 (TREMBLrel. 13, Created)	Q9PSV8 PRELIMINARY;	783
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Q9PSV8 PRELIMINARY;	800 AA.
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	RESULT 7	
DE	FGF receptor_4b.	Q9IXX3	
OS	Xenopus laevis (African clawed frog).	AC	Q9IXX3; PRELIMINARY; PRT; 800 AA.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT	01-OCT-2000 (TREMBLrel. 15, Created)
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;	DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
OC	Xenopoda; Xenopus.	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
NCBI_TAXID	8355; [1]	DE	Fibroblast growth factor receptor receptor 3.
RN	SEQUENCE FROM N.A. Hongo I., Kengaku M., Okamoto H.; "Different employment of FGF signaling system for the embryonic induction." Submitted (SEP-1997) to the EMBL/GemBank/DDJB databases.	GN	FGFR3.
RA	Brachydanio rerio (Zebrafish) (Danio rerio). Eukaryota; Meizaozoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.	OS	

OX	NCBI_TaxID=7955;		
RN [1]	SEQUENCE FROM N.A.; PubMed=11287195;		
RP	Sleptsova-Friedrich I., Li Y., Emelyanov A., Ekker M., Korzh V., Ge R.; "fgfr3 and anteriorization of anterior neural tube in zebrafish.";		
RX	Ge R.; "fgfr3 and anteriorization of anterior neural tube in zebrafish.";		
RA	Nat Mech Dev. 102:213-217(2001).		
RA	DR EMBL; AP157560; AAFB0344.1; -.		
RL	DR HSSP; P11362; IFGK.		
DR	ZFIN; GO:000816-1; fgfr3.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004713; F:protein-tirosine kinase activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:000668; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR03598; Ig-c2.		
DR	InterPro; IPR001245; Tyr_Pkinase.		
DR	PFam; PF00047; ig_3.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	ProDom; PD000001; Prot_kinase.		
DR	SMART; SM00219; SMART_000408; Igc2.		
DR	SMART; SM00219; Tyrkic_1.		
DR	PROSITE; PS50035; IG_LIKE_3.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
KW	ATP-Binding; Immunoglobulin domain; Kinase; Receptor; Transferase;		
KW	Tyrosine-protein kinase.		
SEQUENCE	800 AA; 89716 MW; 8092DC0272ASBAD1 CRC64;		
Query Match	21.2%; Score 464.5; DB 13; Length 800;		
Best Local Similarity	29.2%; Pred. No. 2.3e-32;		
Matches	119; Conservative 84; Mismatches 164; Indels 41; Gaps 11;		
Qy	20 QEKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 REDDADILVYTCSVLFLITMVIIICRWI----NTQTKLTPAPPVQQLSKFKFLKRQV 411		
Qy	74 SWEAGHGNTYALPL-KETSVENFLGATTPLAKLQVPRE-----QLESEVLEQICS 122		
Db	412 SLESNSMNNTPLYVRIASSSDGPMLPNVSELEPSDEPKWEFTRTKLTGLGECCF 471		
Qy	123 GSCGPPIFRAMNTGDPSPKPSVILKEAGLHEVQDFGRIGRIGHQLVQLG 182		
Db	472 GOVMAEAIGIDKEKPKNKLTVAKMLKDGTDXLDSLIVSEMNMKIGHKNINTLG 531		
Qy	183 CCTCTKLPYMLVEDAQGDGLGFWTCRDVMTMGGLYD-----LTERKQVHIG 232		
Db	532 ACTQDGFLIVLVEASKGNREYI-RARPP---PGMDYSFDTCKLIPNETLTPDLYSCA 586		
Qy	233 KOVLLALEPFLQEKHLFHGDVAARNILMOSDLTAKLGLGLAYEVYTRGAISSTOT--IPL 290		
Db	587 YQARGMELYTASRKCCTHRDPAARNLVATEDNVKIADEGLARDVHNDYYKTTNGRLPV 646		
Qy	291 KWLAPERLILRPSIASRADWFSGLLIVNTVLTGAPPYVAPPSTILEHQLQRKXIMKREPS 350		
Db	647 KWMAPEALFDRVYTHQSDLYWSYGULLWEFTLGSPSPYGPVPELFKLLKEGRMDKPN 706		
Qy	351 CTHTMYSIMKSCMRWREADRSPSPRELRLRLEAAIK-TADDEAV-LQVP 3.96		
Db	707 CTHFLYMMBECWHAVPSORSPTRQLVEDHDRVLSMTSTDEYLDLSpV 754		
RESULT	8		
Q91743	PRELIMINARY;		
ID	Q91743, PRELIMINARY;	PRT;	828 AA.
AC	Q91743,		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	FGF receptor 4 precursor.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TAXID=335;		
RN	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96136300; PubMed=5573131;		
RA	Riou J.F., Clavillier L., Boucaut J.C.		
RT	"Early regionalized expression of a novel Xenopus Fibroblast Growth factor receptor in Neuroepithelium,"		
RT	Biochem. Biophys. Res. Commun. 218:198-204 (1996).		
RL			
DR	EMBL; X89807; CNA61930.1; -.		
DR	DR; JC4583; JC4583.		
DR	HSSP; P11362; IFGK.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004713; F:protein-tirosine kinase activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	DR; Ig-1 like.		
DR	InterPro; IPR01110; Ig-c2.		
DR	InterPro; IPR03598; Ig-c2.		
DR	InterPro; IPR00719; Prot_kinase.		
DR	InterPro; IPR01245; Tyr_Pkinase.		
DR	PFam; PF00047; Ig_3.		
DR	PFam; PF00069; Pkinase; 1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	ProDom; PD000001; Prot_kinase.		
DR	SMART; SM00408; Igc2.		
DR	SMART; SM00219; TYRK; 1.		
DR	PROSITE; PS50035; IG_LIKE_3.		
DR	PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
KW	ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal;		
KW	Tyrosine-protein kinase.		
SEQUENCE	800 AA; 89716 MW; 8092DC0272ASBAD1 CRC64;		
Query Match	21.2%; Score 464.5; DB 13; Length 800;		
Best Local Similarity	29.2%; Pred. No. 2.3e-32;		
Matches	119; Conservative 84; Mismatches 164; Indels 41; Gaps 11;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
FT	FT SIGNAL 1 38		
SEQUENCE	828 AA; 93417 MW; 089EB03887603524 CRC64;		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mismatches 170; Indels 32; Gaps 12;		
Qy	21 EKQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Db	357 EKVQEVIIVPTLVTFILLGV1---IWLWFLIREQRTQQRSQP--QGIAFPYPPRDL 73		
Query Match	21.0%; Score 461; DB 13; Length 828;		
Best Local Similarity	29.4%; Pred. No. 4.9e-32;		
Matches	118; Conservative 82; Mism		

RESULT 9		296 ERILLRPASTRADYWSIGLILLYMVTLGAPPVPEVPITSLKQRRKIMKRPSSCHTM 355
Q91742	PRELIMINARY;	
ID	PRT;	818 AA.
AC		
DT	01-JAN-1998 (TREMBLrel. 05, Created)	
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	Fibroblast growth factor receptor-4 precursor.	
OC	Xenopus laevis (African clawed frog).	
NCBI_TaxID	Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopoda; Xenopus.	
OX		
RN	SEQUENCE FROM N.A.	
RP	MEDLINE=95137391; PubMed=7835703;	
RX	Shiozaki C., Tashiro K., Asano-Miyoshi M., Saigo K., Emori Y., Shiokawa K.	
RA	"Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor-4 of Xenopus laevis.";	
RT	Gene 152:215-219(1995); EMBL: D31761; BAA06539.1; -.	
RL	PIR: JC4058; JCA058.	
DR	HSSP; P11362; 1FGK.	
DR	GO; GO:0005224; F:ARP binding; IEA.	
DR	GO; GO:0004113; F:protein-Tyrosine kinase activity; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0016740; F:transferase activity; IEA.	
DR	GO; GO:0004668; P:protein amino acid phosphorylation; IEA.	
DR	InterPro; IPR007119; Ig-like.	
DR	InterPro; IPR003518; Ig-c2.	
DR	InterPro; IPR000719; Prot_kinase.	
DR	InterPro; IPR001245; Tyr_Pkinase.	
DR	InterPro; IPR008266; Tyr_Pkinase_AS.	
PFAM	PF00047; Ig; 3.	
DR	PROSITE; PS50835; Ig_LIKE; 3.	
DR	PROSITE; PS00089; pkinase_1.	
DR	PRINTS; PR00109; TYRKINASE.	
PRODOM	PD000001; Prot_kinase_1.	
SMART	SM00408; IgC2; 3.	
SMART	SM00219; TyrkC; 1.	
DR	PROSITE; PS50835; Ig_LIKE; 3.	
DR	PROSITE; PS000107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	
KW	ATP binding; Immunoglobulin domain; Kinase; Receptor; Signal Transfere; Tyrosine-protein kinase.	
FT	SIGNAL 1 26 MW; POTENTIAL_AA; AB741A5; B8410E41 CRC64;	
SEQUENCE	92065 MW; AB741A5; B8410E41 CRC64;	
Query Match	21.0%; Score 459.5; Length 818;	
Best Local Similarity	29.4%; Pred. No. 6.6e-32;	
Matches 118;	Conservative 83; Mismatches 170; Indels 31; Gaps 11;	
QY	EKQEYVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRAEGYGIEDRPERKPVTVAKMLDNGTDKDLISIEMLKVGKHNNTNLGVST 553	
QY	21 EKQEVIVPT-LIVTIVFLILLGVLWLFIREORTQQRSGPQGIAVPPPPDLSWEAG 78	
DB	376 ESRMDIIYTTSGLAVAMIVIVLCLRMOTPHSKTQLQPAVHKLAFFLIQFSELESS 435	
QY	79 HGGNVALPL-KETSVENFLAGATTPL-----AKLQPREQSEVL-EQICSGSCGP1 128	
DB	436 SSGKSSAPLIRITRSSLSSCAPMLPGYMEVILPDKWEFRDRL-VLGKPLGECCFGQV 493	
QY	129 FRA FRA --NNMTGDPSPKEPKSVILKAKPAGIIEHQYLGKHNVLQLEGCT 185	
DB	494 VRA	

SQ	SEQUENCE	782 AA;	85871 MW;	90262E44POCFE49B CRC64;		DR Pfam; PF00069; pkinase; 1.
	Query Match	20.7%	Score 453.5;	DB 11;	Length 782;	DR PRINTS; PR0109; TYRINKASE.
	Best Local Similarity	30.5%;	Pred. No. 2.1e-3;			DR proDom; PD000001; Prot_kinase; 1.
	Matches	120;	Conservative	71;	Mismatches 165;	DR SMART; SM00408; IGC2; 3.
Qy	34 VTFILLIGVILWLFIREQRTQGQRSGQGIAFP--PPRDLISWEAGHGGNNVALPIKET 90					DR PROSITE; PS50835; IG_LIKE; 3.
Db	357 VVFLFLIVVAAILCRSPPKGLSSPTVKSRPLKRVQLENSSSNSNTBL-V 414					DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
Qy	91 SVENFLGATTTPALA--KLQVP-----REQLVEQICSGSCGPFRANNNTGD 137					DR PROSITE; PS50011; PROTEIN_KINASE_DON; 1.
Db	415 RIARLSSSEGPTVANVSLELPADPKWNLRSRTRLTLGRLGRSCFGQVMMAAIGIDKDR 474					DR ATP-binding; Immunoglobulin domain; Kinase; ATP-binding; Protein Kinase.
Qy	138 PSKPKSVTLLKAKIPEPAGLHEVQDFLGRQFHQYLGKHNLYVQLEGCCTEKPLPYMLVEDV 197					KW Transerase; Tyrosine-protein kinase.
Db	475 TAKPVTAVKMLKDDATDKDSLDSVEMMWMIGKHNINILGACTQGGLPVLYVYA 534					KW SIGNAL 1 20 POTENTIAL.
Qy	198 AQCDLGLLWLTCPDRVMTMDGLY-----DLTEKQVTHIGKQVLLEAFQEKHL 247					FT CHAIN 1 21 800 AA; 87691 MW; B376D47DBB8B312 CRC64;
Db	535 AKGNLREFL-PARRP--PGMDYSFEDACRLPEEQJCKDLYSCAYQVARGMEYLASKC 589					FT CHAIN 800 AA; 87691 MW; B376D47DBB8B312 CRC64;
Qy	248 FHGDVAARNILMOSDLTAKLGLGLAYEVYTRGAISSTQT--IPLKMLAPERILLRPAI 305					SEQUENCE FROM N.A.
Db	590 THRLAAANVNLVTDVNKAIDFLSLARDLTHNLDYKKTTNGRLPVKRNAAPEALFDRTYH 649					SEQUENCE FROM N.A.
Qy	306 RADWWSFSTLLYMVNTLGAAPPYEPVPTSILEHLLQRKIMKRPSSCTHTMYSIMKSCRW 365					SEQUENCE FROM N.A.
Db	650 QSDWWSFGTYLWLWFTLGSSPYPGPVBPFLKULKEGRMRDKDASCTHDLYMIMRECWHA 709					SEQUENCE FROM N.A.
Qy	366 READRPSPRELRLR-AAIKTADEAVLQVP 396					SEQUENCE FROM N.A.
Db	710 VPSQRTPTQVLEDILDTVTSDEYDLSVP 742					SEQUENCE FROM N.A.
	RESULT 13					SEQUENCE FROM N.A.
Q99052	PRELIMINARY;	PRT;	800 AA.			SEQUENCE FROM N.A.
ID	Q99052	PRELIMINARY;	PRT;	800 AA.		SEQUENCE FROM N.A.
AC	Q99052	PRELIMINARY;	PRT;	800 AA.		SEQUENCE FROM N.A.
DT	01-JUN-1998	(TREMBLrel. 06, Created)				SEQUENCE FROM N.A.
DT	01-JUN-2003	(TREMBLrel. 06, Last sequence update)				SEQUENCE FROM N.A.
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)				SEQUENCE FROM N.A.
DE	Fibroblast growth factor receptor.					SEQUENCE FROM N.A.
GN	FGF-2.					SEQUENCE FROM N.A.
OC	Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.					SEQUENCE FROM N.A.
NCBI_TaxID	10090;					SEQUENCE FROM N.A.
RN	[1]					SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.					SEQUENCE FROM N.A.
RC	TISSUE=Skin;					SEQUENCE FROM N.A.
RX	MEDLINE=91296390; PubMed=1648703;					SEQUENCE FROM N.A.
RA	Avivi A., Zimmer Y., Yaron A., Yarden Y., Givol D.; "Errata: Ig-2, a new member of the family of fibroblast growth factor receptors,"; "Flg-2, a new member of the family of fibroblast growth factor receptors [published erratum appears in Oncogene 1992 Apr;7(4):823]."; Oncogene 6:1089-1092 (1991).					SEQUENCE FROM N.A.
RT	"Flg-2, a new member of the family of fibroblast growth factor receptors [published erratum appears in Oncogene 1992 Apr;7(4):823]."; Oncogene 6:1089-1092 (1991).					SEQUENCE FROM N.A.
RL	[2]					SEQUENCE FROM N.A.
DR	EMBL; X58255; CAA41209_1; -.					SEQUENCE FROM N.A.
DR	HSSP; P11362; IFCIK.					SEQUENCE FROM N.A.
DR	MGI; MGI_95524; Fgf3.					SEQUENCE FROM N.A.
DR	GO:0005597; Positive regulation of cell differentiation; IMP.					SEQUENCE FROM N.A.
DR	InterPro; IPR007110; Ig-like.					SEQUENCE FROM N.A.
DR	InterPro; IPR03598; Ig_c2.					SEQUENCE FROM N.A.
DR	InterPro; IPR007119; Prot_kinase.					SEQUENCE FROM N.A.
DR	InterPro; IPR001245; Tyr_Pkinase.					SEQUENCE FROM N.A.
DR	InterPro; IPR008266; Tyr_Pkinase_AS.					SEQUENCE FROM N.A.
DR	Pfam; PF00047; ig_3.					SEQUENCE FROM N.A.

RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.M., Sodergren E.J., Lu X., Gibbs R.A.	[2]
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smilus D.E., Schnier J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RN
RN		SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RA	Straubhaar R.i	RA
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.	RL
DR	EMBL; BC053056; AAH56761; -	DR
SQ	SEQUENCE 800 AA; 87676 MW;	SQ
QY	34 VTFILIGVILWLFIREQRTQOQRSGCPQGIAPV---PPRDL-SWEAGHGENVALPLKET 90	QY
Db	375 VVFLFLIVVAAILCRURSPPKGLGSPTVHKVSFRBLKROVSLNSMSNSNTPL--V 432	Db
QY	91 SVENFLGTTPTAIA---KLQVP-----REQLSEVLQICSGSCGPFRANMNGD 137	QY
Db	433 RARLSSGGEPVIANVSPLELPADPKWELLSRTRLTGLPGLCFCFGVMMAAIGIDKDR 492	Db
QY	138 PSKPKSVIILKALKEPAAGLHEVQDFLGRITQFHQVGLKHNLVQLEGCTERPLMYLVEDV 197	QY
Db	493 TAKPTVAVKMLKDDATKDLSPLVSEMEMMRMIGKHNINILGACTQGGPLVLYVEA 552	Db
QY	198 AQGDLIGFTWTCRVDVMTMDGLY-----DLTEKQVYHIGKQVYLAEFLQEKHL 247	QY
Db	553 AKONLREFL-RARRP---PGMDYSFSDACRLPBEQLTCKDLYSCAYQVARGMByLASQKC 607	Db
QY	248 FHDQDAARNLILMQSDLTAKLGGIGLAYEVYTRGAISSTQT--IPLKWLAPERILLRPASTI 305	QY
Db	608 IHDLAARKNVLTEDDNYKIAFDGLARDHNLDDYKCTTNGRLPVKVNMAPEALFDRYTH 667	Db
QY	306 RADWWSFGILLYEMVTGLAPPYPEVPTTSILEHLQRRKIMRPPSCTHTMSIMKSWRW 365	QY
Db	668 QSWHWSFVLLWELITLGGSPTVGPVPEVTLKLGKHEGRMDKPASCTHDLYMIMRESWHA 727	Db
QY	366 READRPSPELRRLRLE-AAIKTADEAVLQVP 396	QY
Db	728 VPSQRPTEFKQLVEDLDRITVTSDEYLDLSVP 760	Db
RESULT 15		
Q91287	PRELIMINARY; PRT; 796 AA.	Q91287
ID		ID
AC		AC
DT	01-NOV-1996 (TREMBLrel. 01, Created)	DT
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT
DE	Fibroblast growth factor receptor 3.	DE
OS	Pleurodeles wallisi (Iberian ribbed newt).	OS
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Chordata; Salamandroidea; Salamandridae; Pleurodeles.	OC
OC	NCBI_TaxID=8319;	OC
RN	SEQUENCE FROM N.A.	RN
RP	MEDLINE-94289014; PubMed=8026621;	RP
RA	Shi D.L., Launay C., Fromentoux V., Feige J.J., Boucaut J.-C.; "Expression of fibroblast growth factor receptor-2 splice variants is developmentally and tissue-specifically regulated in the amphibian embryo.", Dev. Biol. 164:173-182 (1994).	RA
RT		RT
RT		RT
RT		RT
RL		RL
DR	X75603; CA53271.1; -	DR
DR	PIR; S28579; S28579.	DR
DR	HSSP; P11362; 1RFK.	DR
DR	GO; GO-0005224; F:ATP binding; IEA.	DR
DR	GO; GO-004713; F:protein-tirosine kinase activity; IEA.	DR
DR	GO; GO-1004872; F:receptor activity; IEA.	DR
DR	GO; GO-0016740; F:transfere activity; IEA.	DR
DR	GO; GO-0005668; P:protein amino acid phosphorylation; IEA.	DR
DR	InterPro; IPR07110; Ig-like.	DR
DR	InterPro; IPR03598; Ig_C2.	DR
DR	InterPro; IPR000719; Prot_kinase.	DR
DR	InterPro; IPR01245; Tyr_Pkinase.	DR
DR	InterPro; IPR03266; Tyr_Pkinase_AS.	DR
DR	Pfam; PF00047; Ig_3.	DR
DR	PRINTS; PRO0109; TYRKINASE.	DR
DR	Prodrom; PD000001; Prot_kinase_1.	DR
SMART; SM0040; IgC2; 3.	SMART; SM00219; TyrKc; 1.	SMART; SM0040; IgC2; 3.
DR	PROSITE; PS50835; Ig_LIKE_3.	DR
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.	DR
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	DR
KW	ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase; Tyrosine-protein kinase.	KW
SQ	SEQUENCE 796 AA; 8828 MW;	SQ
226D93A0BD1D92D CRC64;	226D93A0BD1D92D CRC64;	226D93A0BD1D92D CRC64;
Query Match 20.4%; Score 447; DB 13; Length 796;	Query Match 20.4%; Score 447; DB 13; Length 796;	Query Match 20.4%; Score 447; DB 13; Length 796;
Best Local Similarity 28.8%; Pred. No. 8. 2e-31;	Best Local Similarity 28.8%; Pred. No. 8. 2e-31;	Best Local Similarity 28.8%; Pred. No. 8. 2e-31;
Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;	Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;	Matches 112; Conservative 81; Mismatches 166; Indels 30; Gaps 8;
OY	33 LYTFILIGVILWLFIREQRTQOQRSGPOGTAPVPPRDLPSWEAGHGGNYVALPL-KETS 91	OY
Db	368 VAVVILVIIIFTYKMRKMPSKRMNTATVHKVSKFPDKRQVLSLESNSMSNSNTPLVIR 427	Db
QY	92 VENFLAGATTPALAKLQYP-----REQLSEVLQICSGSSCPFRANMNTGDSKP 141	QY
Db	428 LSSSDGPMLANSELPADPKWELSSRSRLTGKPGEGCFQVVMADAVGIGEKKDENKA 487	Db
QY	424 KSVILKALKEPAGLHEVQDFLGRITQFHQVGLKHNLVQLEGCTEKLPLYMWLEDQGD 201	QY
Db	488 TSVAVRMLKDDATKDLSLDSYSEMENKMIGKHNINLIGACTQDGPPLYLVVEYASKGN 547	Db
QY	202 LGFLWTCRRDWTMDGILY-----DLTEKQVYHIGHKQVILALEFLOKHLFHGD 251	QY
Db	548 LREYL-BARRP---PMDDYSPDTCKLDPQEQLTFKDLVSCAQVAREMEYLASQKCTHRD 602	Db
QY	252 VAARNILMOSDLTAKLQGLAYEVYTRGAISSTQT-IPLKWLAPERILLRPASTRADY 309	QY
Db	603 LAARNVLTDDNMVKADFGIAGRDNVNTIDYKTTNGLRPLQWMALFVRVYQSDV 662	Db
QY	310 WSFGILLYEMVTGLAPPYPEVPTTSILEHLQRRKIMRPPSCTHTMSIMKSWRW 365	QY
Db	663 WSFGILLYWFILGSSYPGPVPEELFKLKEGHRMKDPACTHELYMIMRECWHAVPSQ 722	Db
QY	370 RPSPRELRRLRLEAAIK-TADDEAV-LQVP 396	QY
Db	723 RPTFQQLVEDLDRVLTSTDEYLDLSVP 751	Db

Search completed: June 14, 2004, 18:45:44
Job time : 46 secs

[1] SEQUENCE FROM N.A.

Shi D.L., Launay C., Fromentoux V., Feige J.J., Boucaut J.-C.; "Expression of fibroblast growth factor receptor-2 splice variants is developmentally and tissue-specifically regulated in the amphibian embryo.", Dev. Biol. 164:173-182 (1994).

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